



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 174856

TO: Chun Crowder
Location: rem/3B59/3C70
Art Unit: 1644
Wednesday, December 28, 2005
Case Serial Number: 10/780043

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Crowder,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	1163.5	97.9	227	2	Q9UKJ0	HUMAN	Q9ukj0 homo sapien
2	973.5	81.9	203	2	Q9UKJ1	HUMAN	Q9ukj1 homo sapien
3	759	63.8	226	2	Q8NH11	HUMAN	Q8nh11 homo sapien
4	416	35.0	299	2	Q8BYA6	MOUSE	Q8bya6 mus musculus
5	128.5	10.8	823	1	AXL2	YEAST	P38928 saccharomyc
6	123.5	10.4	633	2	Q5W434	BRARE	Q5w434 brachydanio
7	123.5	10.4	651	2	Q5W433	BRARE	Q5w433 brachydanio
8	121	10.2	149	2	Q69YF9	HUMAN	Q69yf9 homo sapien
9	121	10.2	271	2	Q9HBS0	HUMAN	Q9hbs0 homo sapien
10	116.5	9.8	275	2	Q41JCS	GIBBERIA	Q41jcs gibberelia
11	110.5	9.3	245	2	Q65UQ5	MOUSE	Q65uq5 mus musculus
12	109.5	9.2	233	2	Q8TBC9	HUMAN	Q8tbc9 homo sapien
13	109.5	9.2	236	2	Q6PTQ7	HUMAN	Q6ptq7 homo sapien
14	108	9.1	397	1	GATV5	HUMAN	Q6bwxs homo sapien
15	108	9.1	417	2	Q86VU4	HUMAN	Q86vu4 homo sapien
16	106	8.9	403	1	CD33	MOUSE	Q86y94 mus musculus
17	105	8.8	442	2	Q9BY67	HUMAN	Q9by67 homo sapien
18	104	8.7	295	2	Q9Z2H8	MOUSE	Q9z2h8 mus musculus
19	104	8.7	445	2	Q8R4L1	MOUSE	Q8r4l1 mus musculus
20	103.5	8.7	359	2	Q5RLX6	RAT	Q5rlx6 rattus norv
21	103	8.7	233	2	Q6PJ3	HUMAN	Q6pia3 homo sapien
22	102	8.6	240	1	CD48	MOUSE	P18181 mus sapien
23	102	8.6	240	2	Q545K2	MOUSE	Q545k2 mus musculus
24	102	8.6	240	2	Q6P905	MOUSE	Q6p905 mus musculus
25	102	8.6	283	2	Q5DWN5	EPTBU	Q5dwn5 eptatretus
26	102	8.6	283	2	Q5DWN6	EPTBU	Q5dwn6 eptatretus
27	102	8.6	370	2	Q4KCS	PSRFP5	Q4kcs pseudomonas
28	101.5	8.5	151	2	Q8CZT1	MOUSE	Q8czt1 mus musculus
29	101.5	8.5	237	2	Q6DHW4	HUMAN	Q6dhw4 homo sapien
30	101.5	8.5	359	1	HPLN3	MOUSE	Q80wm5 mus musculus
31	101.5	8.5	369	2	Q7YUQ4	9TRYP	Q7yvu4 trypanosoma

[illegible]

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Db 121 SVYFCRVELDTRRGRQLOQSIKTKLTITQAVTTTTTWRPSSTTIAGLRVTSKGHSE 180
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Db 181 SWHLSLDTAIRVALAVAKTVIIGLLC-LLLMWRRRKGSRAPSSDF 227

RESULT 2
Q9UKJ1 HUMAN
ID Q9UKJ1 HUMAN PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DB Inhibitory receptor PILRALpha.
GN Name=PILRA;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
paired with the truncated counterpart PILRBeta.";
RL J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161080; AAD2964.1; -; mRNA.
DR Ensembl; ENSG00000085514; Homo sapiens.
DR HGNC; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 303 AA; 33878 MW; 0410ADFCE80928B CRC64;

Query Match 81.9%; Score 973.5; DB 2; Length 303;
Best Local Similarity 82.5%; Pred. No. 1.9e-80;
Matches 188; Conservative 14; Mismatches 17; Indels 9; Gaps 2;

Qy 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
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Db 121 SVYFCRVELDTRRGRQLOQSIKTKLTITQAVTTTTTWRPSSTTIAGLRV 180
Qy 173 TESKGHSSSWHLSLDTAIRVALAVAKTVIIGLLC-LLLMWRRRKGSR 220
Db 181 TQGRKRSWSWHLSLDTAIRVALAVAKTVIIGLLC-LLLMWRRRKGSR 227

RESULT 3
Q8NH11 HUMAN
ID Q8NH11 HUMAN PRELIMINARY; PRT; 226 AA.
AC Q8NH11;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PILRA protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krawinski M.I., Skalek U., Smailus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017812; AAH17812.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;

Query Match 63.8%; Score 759; DB 2; Length 226;
Best Local Similarity 88.3%; Pred. No. 5.1e-61;
Matches 143; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

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Qy 61 LATAPDVIRISWRGRGHFGQSFYSTRPSPSIHKDYNNRFLNLTWTEQSGSGLRISNLRKEDQ 120
Db 61 LATAPDVIRISWRGRGHFGQSFYSTRPSPSIHKDYNNRFLNLTWTEQSGSGLRISNLRKEDQ 120
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Db 121 SVYFCRVELDTRRGRQLOQSIKTKLTITQAVTTTTTWRPSS 162

RESULT 4
Q8BYA6 MOUSE
ID Q8BYA6 MOUSE PRELIMINARY; PRT; 299 AA.
AC Q8BYA6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630007P20 product:weakly similar to INHIBITORY
DE RECEPTOR PILRALPHA.
GN Name=Pilra; Synonyms=AV021745;
OS Mus musculus (Mouse).
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 23.5538 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-10
Perfect score: 1189
Sequence: 1 MGRPILLPLLLQLQPPAFLO.....LCLLLWRRRKGSRAPSSDF 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfilees1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1189	100.0	226	2	US-09-869-388-10
2	1163.5	97.9	227	2	US-09-869-388-6
3	1067	89.7	238	2	US-09-149-476-485
4	973.5	81.9	303	2	US-08-985-950-2
5	973.5	81.9	303	2	US-09-546-049-2
6	973.5	81.9	303	2	US-09-869-388-2
7	759	63.8	230	2	US-09-869-388-4
8	757.5	63.7	175	2	US-09-869-388-8
9	534	44.9	101	2	US-09-149-476-754
10	226	19.0	99	2	US-08-985-950-4
11	226	19.0	99	2	US-09-546-049-4
12	115.5	9.7	310	2	US-09-079-029-11
13	114.5	9.6	244	2	US-08-918-148-79
14	114.5	9.6	244	2	US-09-138-091A-77
15	114	9.6	352	2	US-09-203-958A-2
16	112	9.4	476	2	US-09-291-299A-3
17	109	9.2	143	1	US-08-345-321-8
18	107	9.0	355	2	US-08-875-811-57
19	105.5	8.9	622	1	US-08-356-786-16
20	105	8.8	440	2	US-09-866-028-61
21	105	8.8	440	2	US-09-944-457-61
22	105	8.8	440	2	US-09-945-584-61
23	105	8.8	440	2	US-09-944-944-61
24	105	8.8	440	2	US-09-945-587-61
25	105	8.8	442	2	US-09-778-510-20
26	105	8.8	442	2	US-09-930-803-1
27	104	8.7	265	1	US-08-403-853-16

28	104	8.7	423	2	US-09-778-510-22	Sequence 22, Appl
29	103	8.6	460	2	US-10-630-406-5	Sequence 5, Appl
30	102.5	8.6	421	2	US-08-759-628-5	Sequence 5, Appl
31	101.5	8.5	284	2	US-08-564-164A-2	Sequence 2, Appl
32	101.5	8.5	551	2	US-08-896-537A-2	Sequence 2, Appl
33	100	8.4	159	1	US-08-653-402B-2	Sequence 2, Appl
34	100	8.4	300	1	US-08-661-052-4	Sequence 4, Appl
35	100	8.4	300	2	US-09-188-082-4	Sequence 4, Appl
36	100	8.4	300	2	US-09-364-088-4	Sequence 4, Appl
37	100	8.4	300	2	US-09-102-716-4	Sequence 4, Appl
38	100	8.4	312	2	US-09-079-029-10	Sequence 10, Appl
39	100	8.4	354	2	US-09-393-627B-28	Sequence 28, Appl
40	100	8.4	360	2	US-09-907-794A-213	Sequence 213, App
41	100	8.4	360	2	US-09-905-125A-213	Sequence 213, App
42	100	8.4	360	2	US-09-902-775A-213	Sequence 213, App
43	100	8.4	360	2	US-09-906-700-213	Sequence 213, App
44	100	8.4	360	2	US-09-903-603A-213	Sequence 213, App
45	100	8.4	360	2	US-09-904-920A-213	Sequence 213, App

ALIGNMENTS

RESULT 1
US-09-869-388-10
; Sequence 10, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IEM PC compatible
; SEQ ID NO 10
; LENGTH: 226
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-10

Query Match 100.0%; Score 1189; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.4e-107;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGRPILLPLLLQLQPPAFLOPGGSGPSYLYGVTPKHLASMGSGSVEIPFSFYYPWE 60
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DB 61 LATAPDVRIWRRGHFHQGSFYSTRPPSIHKDYNNRFLNWTGEGSGFLRISNLRKEDQ 120
QY 121 SYVFCRVELDRSRGRQQLQSIKGTKLITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
DB 121 SYVFCRVELDRSRGRQQLQSIKGTKLITQAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
QY 181 SWHLSLDTAIRVALAVAVLKVTLGLCLLLWRRRKGSRAPSSDF 226
DB 181 SWHLSLDTAIRVALAVAVLKVTLGLCLLLWRRRKGSRAPSSDF 226

RESULT 2
US-09-869-388-6
; Sequence 6, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel

APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS

FILE REFERENCE: S80977X
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 6
LENGTH: 227
TYPE: PRT
ORGANISM: homo sapiens
US-09-869-388-6

Query Match 97.9%; Score 1163.5; DB 2; Length 227;
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Matches 223; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
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Db 61 LAIVNVRISWRGHFGQSPYSTRPSPSIHKDYVNRFLPLNWTGQSGFLRISNLRKEDQ 120
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Db 121 SVYFCRVELDTRRGRQQLQIKGTITITCAVTTTTTWRPSSTTTIAGLRVTSKGHSE 180
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Db 181 SWHLSLDTAIRVALAVLKTIVILGLLCLLLMWRRRKGRAPSSDF 227

RESULT 3

US-09-149-476-485
Sequence 485, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
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EARLIER APPLICATION NUMBER: 60/040,163
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/047,600
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,615
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EARLIER APPLICATION NUMBER: 60/047,597
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EARLIER APPLICATION NUMBER: 60/047,502
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EARLIER APPLICATION NUMBER: 60/047,601
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EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
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EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:41:30 ; Search time 4.28252 Seconds
(without alignments)
376.418 Million cell updates/sec

Title: US-10-780-043-10
Perfect score: 1189
Sequence: 1 MGRPLLLPLLLLQPPAPLQ.....LCLLWRRKGRAPSSDF 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	9.6	250	US-10-512-184-27	Sequence 27, Appl
2	111	9.3	250	US-11-054-515-2073	Sequence 2073, Ap
3	110.5	9.3	256	US-11-054-515-907	Sequence 907, App
4	109	9.2	258	US-10-512-184-26	Sequence 26, Appl
5	109	9.2	327	US-10-512-184-62	Sequence 62, Appl
6	109	9.2	327	US-10-512-184-64	Sequence 64, Appl
7	109	9.2	328	US-10-512-184-63	Sequence 63, Appl
8	109	9.2	576	US-10-512-184-65	Sequence 65, Appl
9	109	9.2	625	US-10-512-184-47	Sequence 47, Appl
10	108.5	9.1	250	US-11-054-515-1319	Sequence 1319, Ap
11	108	9.1	250	US-11-054-515-2095	Sequence 2095, Ap
12	107.5	9.0	246	US-11-054-515-2079	Sequence 2079, Ap
13	106.5	9.0	252	US-11-054-515-897	Sequence 897, App
14	106.5	9.0	252	US-11-054-515-1016	Sequence 1016, Ap
15	106.5	9.0	252	US-11-054-515-1131	Sequence 1131, Ap
16	106.5	9.0	252	US-11-054-515-1135	Sequence 1135, Ap
17	106.5	9.0	252	US-11-054-515-1163	Sequence 1163, Ap
18	106.5	9.0	254	US-11-054-515-1893	Sequence 1893, Ap
19	106	8.9	242	US-11-054-515-1884	Sequence 1884, Ap
20	106	8.9	250	US-11-054-515-3247	Sequence 3247, Ap
21	105.5	8.9	252	US-11-054-515-1787	Sequence 1787, Ap
22	104.5	8.8	245	US-11-054-515-1946	Sequence 1946, Ap
23	104.5	8.8	247	US-11-054-515-1751	Sequence 1751, Ap
24	104.5	8.8	248	US-11-054-515-1617	Sequence 1617, Ap
25	104.5	8.8	251	US-11-054-515-1669	Sequence 1669, Ap

ALIGNMENTS

RESULT 1
US-10-512-184-27
; Sequence 27, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"derung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 27
; LENGTH: 250
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with
; OTHER INFORMATION: specificity against Fusarium spp.; originates from
; OTHER INFORMATION: Gallus gallus.
US-10-512-184-27

Query Match 9.6%; Score 114; DB 6; Length 250;
Best Local Similarity 31.0%; Pred. No. 0.0005;
Matches 35; Conservative 20; Mismatches 30; Indels 28; Gaps 6;
QY 21 PG-GSTGSPVLYGVCTOPKHLASMGSGSVETPPS---FYYPWEL---ATAPDVRISWR 72
DB 134 PEGSTGKAPA---LTQFPSSVSNALGTVKTCSTGSHYSHWQKSPGSPAVTLI--- 186
QY 73 RGHFHGQFYSTRPDSIHKVYVNRFLNWTQEGSGFLRISNLKRDQSVYFC 125
DB 187 -----SFNNORPDSIPSRP-----SGSKSGSGTGLTITGVRAEDAVYIC 226

RESULT 2

US-11-054-515-2073
; Sequence 2073, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296

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; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2073
; LENGTH: 250
; TYPE: PRP
; ORGANISM: Homo sapiens
US-11-054-515-2073

Query Match          9.3%; Score 111; DB 7; Length 250;
Best Local Similarity 26.4%; Pred. No. 0.00097;
Matches 47; Conservative 24; Mismatches 57; Indels 50; Gaps 9;

Qy 46 GGSVEI-----PSPYYPWELATAPDVRSRGRHF--HGQSFYSTRPPSTHKDYVN 95
Db 15 GSSVKVCKASGGTFSSYALSWVRQAPQGQLEW-MGIPPIFGTEYYAER-----FQG 66
Qy 96 RLFLNWTGEGSGFLRISNLAKEQSVVFC-RVELDTRRSRQQLQSIKGTPLTIT--- 150
Db 67 RVTITADESTWATYLDLSLSESDATVYVCARVDYTDYMGAFDLWG-QGTLVTVSSGGG 125
Qy 151 -----QAVYTTTWRPSSTTTIAGLRVTE-----KGHSSEWHLSL 186
Db 126 GSGGGGGGGGSAQAVLT-----QPSVSGARGQRTTISCTGSSNIGAGYDVHYYQQL 179

RESULT 3
US-11-054-515-907
; Sequence 907, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR APPLICATION NUMBER: 60/240,816
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; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 907
; LENGTH: 256
; TYPE: PRP
; ORGANISM: Homo sapiens
US-11-054-515-907

Query Match          9.3%; Score 110.5; DB 7; Length 256;
Best Local Similarity 29.1%; Pred. No. 0.0011;
Matches 41; Conservative 20; Mismatches 45; Indels 35; Gaps 8;

Qy 22 GGSTGSPSYLYGVTPQKHLASMGSGSVETPFPFPYPMELATAPDV-----RISWRGRHF 77
Db 136 GGSGGGGSAQALTPASVSGSGSITISCT-----GTSSDVGRYVYVSWYR-QYP 187
Qy 78 GQS-----FYS--TRPPSIHKDYVNRFLNWTGEGSG---FLRISNLRKEDQSVYFCRVE 128
Db 188 GEAPKLMYGVINRPSGVSSRP-----SGSKSGNTASLTISGLQADEADYFC--- 235
Qy 129 LDTRRSGRQQLQSIKGTPLTIT 149
Db 236 --SSYAGRSTYVFGTKVTV 254

RESULT 4
US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 258
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv CWP2
; OTHER INFORMATION: with specificity against Fusarium spp.; originates
; OTHER INFORMATION: from Gallus gallus.
US-10-512-184-26

Query Match          9.2%; Score 109; DB 6; Length 258;
Best Local Similarity 31.2%; Pred. No. 0.0016;
Matches 44; Conservative 18; Mismatches 43; Indels 36; Gaps 9;

Qy 21 PG-GSTGSPSYLYGVTPQKHLASMGSGSVETPFPFPYPM-----ELATAPDVRSWR 72
Db 138 PEGSTKGAPA-----LTQPSVSVANLGTVEITCGGGYRYGWQQSPGSAPTVYVW- 192
Qy 73 RGHFHGQSFYSTRPPSIHKDYVNRFLNWTGEGSG---FLRISNLRKEDQSVYFCRVEL 129
Db 193 -----DDDSANRPSNIPSRP-----SGSTSGSTATITITGVQADDEAVYFCGSY- 236
Qy 130 DTRASGRQQLQSIKGTPLTIT 150
Db 237 -DRSSG---YVSIFGAGTTLT 253

RESULT 5
US-10-512-184-62
; Sequence 62, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:40:10 ; Search time 76.8906 Seconds
(without alignments)
1228.101 Million cell updates/sec

Title: US-10-780-043-10
Perfect score: 1189
Sequence: 1 MGRPILLPILLLOPPAFLO.....LCILLWRRKGRAPSDP 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 41782326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1189	100.0	226	3	US-09-774-381-44
2	1189	100.0	226	4	US-10-780-043-10
3	1183	99.5	226	3	US-09-745-763-106
4	1163.5	97.9	227	4	US-10-262-445-128
5	1163.5	97.9	227	4	US-10-780-043-6
6	1163.5	97.9	227	5	US-10-820-474A-7
7	1163.5	97.9	291	3	US-09-935-390A-21
8	1163.5	97.9	326	4	US-10-276-774-2380
9	1067	89.7	238	3	US-09-809-391-485
10	1067	89.7	238	3	US-09-882-171-485
11	1067	89.7	238	4	US-10-164-861-485
12	973.5	81.9	303	3	US-09-774-381-58
13	973.5	81.9	303	4	US-10-290-631-2
14	973.5	81.9	303	4	US-10-780-043-2
15	973.5	81.9	303	4	US-10-777-524-2
16	973.5	81.9	303	5	US-10-777-521-2
17	765	64.3	1012	5	US-10-450-763-30868
18	765	64.3	1012	5	US-10-450-763-33210
19	765	64.3	1012	5	US-10-450-763-47228
20	765	64.3	1012	5	US-10-450-763-51762
21	759	63.8	230	4	US-10-309-290-110
22	759	63.8	230	4	US-10-780-043-4
23	757.5	63.7	206	4	US-10-780-043-8
24	598	50.3	175	4	US-10-309-290-112
25	534	44.9	101	3	US-09-809-391-754
26	534	44.9	101	3	US-09-882-171-754
27	534	44.9	101	4	US-10-164-861-754

28	377	31.7	224	3	US-09-866-050A-711	Sequence 711, App
29	226	19.0	99	4	US-10-290-631-4	Sequence 4, Appli
30	226	19.0	99	4	US-10-777-524-4	Sequence 4, Appli
31	226	19.0	99	5	US-10-777-521-4	Sequence 4, Appli
32	122.5	10.3	257	4	US-10-270-073-8	Sequence 8, Appli
33	121.5	10.2	124	5	US-10-788-625-92	Sequence 92, Appli
34	121.5	10.2	253	4	US-10-479-670-174	Sequence 174, App
35	121	10.2	256	4	US-10-270-073-6	Sequence 6, Appli
36	116	9.8	252	4	US-10-479-670-168	Sequence 168, App
37	115.5	9.7	310	4	US-10-052-798-11	Sequence 11, Appl
38	115.5	9.7	310	4	US-10-288-917-11	Sequence 11, Appl
39	115.5	9.7	310	4	US-10-423-448-11	Sequence 11, Appl
40	115.5	9.7	448	4	US-10-378-567-2	Sequence 2, Appli
41	115	9.7	253	4	US-10-479-670-184	Sequence 184, App
42	114.5	9.6	244	5	US-10-778-394-77	Sequence 77, Appl
43	114.5	9.6	261	4	US-10-270-071-18	Sequence 18, Appl
44	114.5	9.6	261	4	US-10-270-073-2	Sequence 2, Appli
45	114.5	9.6	261	4	US-10-328-190-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-774-381-44
; Sequence 44, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNT-107CP2
; CURRENT APPLICATION NUMBER: US/09774,381
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 44
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 100.0%; Score 1189; DB 3; Length 226;
Best Local Similarity 100.0%; Pred. No. 8.5e-99;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MGRPILLPILLLOPPAFLOPGSGPSYLYGVTPKLSMKGSGVEIFPSFYWE 60
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Db 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Qy 61 LATAPDVRIWRGHHFGHQSFSYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Db 61 LATAPDVRIWRGHHFGHQSFSYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTIQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
Db 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTIQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVAVLTKTVILGLCLLLWRRRRKGRAPSSDF 226
Db 181 SWHLSLDTAIRVALAVAVLTKTVILGLCLLLWRRRRKGRAPSSDF 226

RESULT 2
US-10-780-043-10
; Sequence 10, Application US/10780043
; Publication No. US20040137506A1
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/10/780,043
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/869,389
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 10
; LENGTH: 226
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-780-043-10

Query Match 100.0%; Score 1189; DB 4; Length 226;
Best Local Similarity 100.0%; Pred. No. 8.5e-99;
Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Qy 61 LATAPDVRIWRGHHFGHQSFSYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Db 61 LATAPDVRIWRGHHFGHQSFSYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTIQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
Db 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTIQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVAVLTKTVILGLCLLLWRRRRKGRAPSSDF 226
Db 181 SWHLSLDTAIRVALAVAVLTKTVILGLCLLLWRRRRKGRAPSSDF 226

RESULT 3
US-09-745-763-106
; Sequence 106, Application US/09745763
; Patent No. US20020065394A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaValle, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Marberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
```

```
; ; ENCODING THEM
; ;
; ; NUMBER OF SEQUENCES: 219
; ; CORRESPONDENCE ADDRESS:
; ; ADDRESSEE: Genetics Institute, Inc.
; ; STREET: 87 Cambridgepark Drive
; ; CITY: Cambridge
; ; STATE: MA
; ; COUNTRY: U.S.A.
; ; ZIP: 02140
; ; COMPUTER READABLE FORM:
; ; MEDIUM TYPE: Floppy disk
; ; COMPUTER: IBM PC compatible
; ; OPERATING SYSTEM: PC-DOS/MS-DOS
; ; SOFTWARE: PatentIn Release #1.0, Version #1.30
; ; CURRENT APPLICATION DATA:
; ; APPLICATION NUMBER: US/09/745,763
; ; FILING DATE: 18-Jun-2000
; ; CLASSIFICATION: <Unknown>
; ; ATTORNEY/AGENT INFORMATION:
; ; NAME: Sprunger, Suzanne A.
; ; REGISTRATION NUMBER: 41,323
; ; TELECOMMUNICATION INFORMATION:
; ; TELEPHONE: (617) 498-8284
; ; TELEFAX: (617) 876-5851
; ; INFORMATION FOR SEQ ID NO: 106:
; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 226 amino acids
; ; TYPE: amino acid
; ; STRANDEDNESS: <Unknown>
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
; ; SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-09-745-763-106

Query Match 99.5%; Score 1183; DB 3; Length 226;
Best Local Similarity 99.6%; Pred. No. 2.9e-98;
Matches 225; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Qy 61 LATAPDVRIWRGHHFGHQSFSYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Db 61 LATAPDVRIWRGHHFGHQSFSYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTIQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
Db 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTIQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVAVLTKTVILGLCLLLWRRRRKGRAPSSDF 226
Db 181 SWHLSLDTAIRVALAVAVLTKTVILGLCLLLWRRRRKGRAPSSDF 226

RESULT 4
US-10-262-445-128
; Sequence 128, Application US/10262445
; Publication No. US20040014058A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
; APPLICANT: Burgess, Catherine
; APPLICANT: Catterton, Elina
; APPLICANT: Chant, John
; APPLICANT: Chaudhuri, Amitabha
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gerlach, Valerie
; APPLICANT: Giot, Loic
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Mezes, Peter
; APPLICANT: Millet, Isabelle
```

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:18:33 ; Search time 94.0207 Seconds
(without alignments)
1056.147 Million cell updates/sec

Title: US-10-780-043-10
Perfect score: 1189
Sequence: 1 MGRPLLLLLLLLQPPAFQ.....LCLLLWRRKGRAPSSDP 226

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1189	100.0	226	2 AAY08015	Human LSP
2	1189	100.0	226	2 AAB07447	A human m
3	1183	99.5	226	2 AAW80407	A secret
4	1183	99.5	226	5 ABP61825	Human pol
5	1163.5	97.9	227	3 AAB07445	A human m
6	1163.5	97.9	227	6 ABU89824	TNF-recep
7	1163.5	97.9	291	2 AAW63682	Human sec
8	1163.5	97.9	326	4 ABB12010	Human sec
9	1150.5	96.8	227	3 AAY87230	Human sig
10	1067	89.7	238	5 ABG95345	Human nov
11	1067	89.7	238	6 ABG03453	Region of
12	1067	89.7	238	7 AD123200	Novel hum
13	1067	89.7	238	8 ADH74202	Human imm
14	973.5	81.9	303	2 AAW62772	Human imm
15	973.5	81.9	303	3 AAB07443	A human m
16	973.5	81.9	303	8 ADP25129	PRO polyp
17	765	64.3	1012	4 ABG00509	Novel hum
18	765	64.3	1012	4 ABG16869	Novel hum
19	765	64.3	1012	4 ABG02851	Novel hum
20	765	64.3	1012	4 ABG21403	Novel hum
21	759	63.8	228	8 ADK98565	Human imm
22	759	63.8	230	3 AAB07444	A human m
23	759	63.8	230	7 ADP25578	Human NOV
24	757.5	63.7	175	3 AAB07446	A human m

25	598	50.3	206	7	ADP95580	Human NOV
26	534	44.9	101	2	AAW75053	Fragment
27	534	44.9	101	5	ABG95614	Human nov
28	534	44.9	101	6	ABO34808	Fragment
29	534	44.9	101	7	ADI23469	Novel hum
30	534	44.9	101	8	ADH74471	Human sec
31	377	31.7	224	5	ABH72387	Murine pr
32	369.5	31.1	212	2	ABE59537	Rat Prote
33	226	19.0	99	2	AAW62773	Partial m
34	122.5	10.3	257	6	ABR42758	Anti-CEA
35	122	10.3	253	6	AAU19873	Activatin
36	121.5	10.2	253	6	ABU97134	Recombina
37	121	10.2	256	6	ABR42757	Anti-CEA
38	121	10.2	271	5	AAU72792	Human ant
39	116.5	9.8	555	4	AAU19871	Activatin
40	116	9.8	252	6	ABU97128	Recombina
41	115.5	9.7	310	2	AAW83324	Single ch
42	115.5	9.7	310	5	ABB09605	Amino aci
43	115.5	9.7	310	6	ABG74386	Single ch
44	115.5	9.7	310	7	ADG98739	Human sin
45	115.5	9.7	310	8	ADO40448	Human sin

ALIGNMENTS

RESULT 1

AAAY08015
ID AAY08015 standard; protein; 226 AA.

XX AC AAY08015;

XX DT 08-JUL-1999 (first entry)

XX DE Human LSP-1 protein.

XX KW LSP-1; signal peptide; leucocyte-specific protein-1; PA-I; TAP-1; cancer; proliferin analogue 1; thrombopoietin analogue protein 1; anticancer; antiangiogenic; anticancer; anti-inflammatory; anti-thrombocytopenic; anti-arthritis; signal transduction; inflammatory; disease; growth; proliferation; differentiation; cell survival; angiogenesis; diagnosis; haematopoietic stem cell; erythroid precursor; megakaryocytopenia; thrombocytopenia; prognosis; treatment; chromosome mapping; tissue typing; forensic; arthritis; thrombocytopenia; bone marrow transplant; infection; intravascular coagulation; iron deficiency; HIV; human.

XX OS Homo sapiens.

XX PN WO9918243-A1.

XX XX 15-APR-1999.

XX PP 06-OCT-1998; 98WO-US021151.

XX PR 06-OCT-1997; 97US-0061143P.

XX PR 06-OCT-1997; 97US-0061149P.

XX PR 06-OCT-1997; 97US-0061159P.

XX PR 08-JAN-1998; 98US-00004206.

XX PR 22-JAN-1998; 98US-00010674.

XX PR 27-JAN-1998; 98US-00014347.

XX XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX PI Pan Y, Gearing DP, McCarthy SA;

XX DR WPI: 1999-264042/22.

XX DR N-PSDB; AAX37558.

XX PT Signal-peptide containing proteins that modulate cellular processes.

XX PS Claim-2; Fig 1; 124pp; English.

XX CC This invention describes the isolation of nucleic acids encoding the

CC signal-peptide-containing molecules leucocyte-specific protein-1 (LSP-1),
 CC proliferin analog I (PA-I) and thrombopoietin analog protein 1 (TAP-1).
 CC These proteins have antiangiogenic, anticancer, anti-inflammatory, anti-
 CC atheritic and anti-thrombocytopenic activity. The products of the
 CC inflammation and their modulators are involved in signal transduction,
 CC inflammatory responses, growth, proliferation, differentiation and
 CC survival of cells; angiogenesis; maturation of haematopoietic stem cells
 CC and erythroid precursors megakaryocytopoiesis and thrombopoiesis.
 CC Antibodies, or other binding agents, specific for the products of the
 CC invention are useful for diagnosis, prognosis and monitoring of treatment
 CC of diseases. Other uses include chromosome mapping, identification of
 CC individuals (tissue typing) and in forensic studies. LSP-1, PA-I and TAP-
 CC 1 proteins and nucleic acids are modulators of cellular processes,
 CC particularly they are used to treat or prevent diseases associated with
 CC deregulation of angiogenesis, immune responses and hematopoiesis, e.g.
 CC cancer, arthritis (and other inflammatory diseases), thrombocytopenia
 CC (caused by cancer treatment, bone marrow transplant, human immune
 CC deficiency virus infection etc.), intravascular coagulation, iron
 CC deficiency etc

XX Sequence 226 AA;

Query Match 100.0%; Score 1189; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.7e-95;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLLQPPAFLOPGSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
 Db 1 MGRPLLLPLLLLLQPPAFLOPGSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
 Qy 61 LATAPDVRIWRRGHFGQSFYSTRPPIHKDYVNRFLNWTGQSGFLRISNLRKEDQ 120
 Db 61 LATAPDVRIWRRGHFGQSFYSTRPPIHKDYVNRFLNWTGQSGFLRISNLRKEDQ 120
 Qy 121 SVYFCRVELDTRRSGRQLOQSIKGTCLTITQAVTTTTTWRPSSTTTTLGLRVTSKGHSE 180
 Db 121 SVYFCRVELDTRRSGRQLOQSIKGTCLTITQAVTTTTTWRPSSTTTTLGLRVTSKGHSE 180
 Qy 181 SWHLSLDTAIRVALAVAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 226
 Db 181 SWHLSLDTAIRVALAVAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 226

RESULT 2
 AAB07447
 ID AAB07447 standard; protein; 226 AA.
 AC AAB07447;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE A human monocyte-derived protein FDF03-S2.
 XX
 KW Human; monocyte-derived protein; FDF03; FDF03deltaTM; FDF03-S1;
 KW FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
 KW tissue rejection; inflammation; infection.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..17
 FT /note= "signal sequence"
 FT Protein 18..226
 FT /note= "mature protein"

XX WO200040721-A1.
 XX 13-JUL-2000.
 XX
 XX 29-DEC-1999; 99WO-US030004.
 XX
 PR 31-DEC-1998; 98US-00223919.
 PR 31-DEC-1998; 98US-00224604.

XX (SCHE) SCHERING CORP.

XX Bates E, Fournier N, Chaulus L, Garrone P;

XX WPI; 2000-465984/40.

XX N-PSDB; AAA58818.

XX Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
 PT diseases associated with changes in monocyte numbers, e.g. bacterial or
 FT viral infections.

XX Claim 1; Page 41-42; 45pp; English.

XX The present sequence represents a human monocyte-derived protein. The
 CC specification describes monocyte-derived proteins FDF03, FDF03deltaTM,
 CC FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
 CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocyte-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocyte hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX Sequence 226 AA;

Query Match 100.0%; Score 1189; DB 3; Length 226;
 Best Local Similarity 100.0%; Pred. No. 1.7e-95;
 Matches 226; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLLQPPAFLOPGSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
 Db 1 MGRPLLLPLLLLLQPPAFLOPGSGTSGPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
 Qy 61 LATAPDVRIWRRGHFGQSFYSTRPPIHKDYVNRFLNWTGQSGFLRISNLRKEDQ 120
 Db 61 LATAPDVRIWRRGHFGQSFYSTRPPIHKDYVNRFLNWTGQSGFLRISNLRKEDQ 120
 Qy 121 SVYFCRVELDTRRSGRQLOQSIKGTCLTITQAVTTTTTWRPSSTTTTLGLRVTSKGHSE 180
 Db 121 SVYFCRVELDTRRSGRQLOQSIKGTCLTITQAVTTTTTWRPSSTTTTLGLRVTSKGHSE 180
 Qy 181 SWHLSLDTAIRVALAVAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 226
 Db 181 SWHLSLDTAIRVALAVAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 226

RESULT 3
 AAW80407
 ID AAW80407 standard; protein; 226 AA.

XX AAW80407;

XX 25-MAR-2003 (revised)
 DT 13-JAN-1999 (first entry)

XX A secreted protein encoded by clone di39_9.

XX Secreted protein; immune stimulating; suppressing;
 KW haematopoiesis regulating activity; tissue growth activity; activin;
 KW inhibit activity; chemotactic; chemokinetic activity; haemostatic;
 KW thrombolytic activity; anti-inflammatory activity; cadherin;
 KW tumour invasion suppressor activity; tumour inhibition activity.

XX Homo sapiens.

XX WO9844113-A1.

XX 08-OCT-1998.

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	934	100.0	175	3	AAB07446	Aab07446 A 1
2	821	87.9	303	2	Aaw62772	Aaw62772 Hun
3	821	87.9	303	3	AAB07443	Aab07443 A 1
4	821	87.9	303	8	ADP25129	ADp25129 PRG
5	816	87.4	228	8	ADK98565	Adk98565 Hun
6	816	87.4	230	3	AAB07444	Aab07444 A 1
7	816	87.4	230	7	ADE95578	AdE95578 Hun
8	809.5	86.7	1012	4	ABG00509	ABg00509 NOV
9	809.5	86.7	1012	4	ABG16869	ABg16869 NOV
10	809.5	86.7	1012	4	ABG02851	ABg02851 NOV
11	809.5	86.7	1012	4	ABG21403	ABg21403 NOV
12	757.5	81.1	226	2	Aaw80407	Aaw80407 A 1
13	757.5	81.1	226	2	AAy08015	Aay08015 Hun
14	757.5	81.1	226	3	AAY08017	Aay08017 A 1
15	757.5	81.1	226	5	ABP61825	ABp61825 Hun
16	743.5	79.6	238	5	ABG95345	ABg95345 Hun
17	743.5	79.6	238	6	ABO34539	ABo34539 Reg
18	743.5	79.6	238	7	ADi123200	ADi123200 NOV
19	743.5	79.6	238	8	ADH74202	ADh74202 Hun
20	742.5	79.5	227	3	AAB07445	Aab07445 A 1
21	742.5	79.5	227	6	ABU89824	ABu89824 TNE
22	742.5	79.5	291	2	AAW63682	Aaw63682 Hun
23	742.5	79.5	326	4	ABBI12010	ABb12010 Hun
24	729.5	78.1	227	3	AAy87230	Aay87230 Hun

CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocytic-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocytic hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX SQ Sequence 175 AA;

Query Match 100.0%; Score 934; DB 3; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.4e-80;
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPPLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Db 1 MGRPLLLPPLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Qy 61 LATAPDVRIWRGHFHGQSFYSTRPPSIHKDYVNRFLNWTGQSGFLRISNLOKQDQ 120
 Db 61 LATAPDVRIWRGHFHGQSFYSTRPPSIHKDYVNRFLNWTGQSGFLRISNLOKQDQ 120
 Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTQSHRISGMKDKIQIPS 175
 Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTQSHRISGMKDKIQIPS 175

RESULT 2

AAW62772
 ID AAW62772 standard; protein; 303 AA.

XX AC AAW62772;

XX DT 23-SEP-1998 (first entry)

XX DE Human immunoglobulin receptor designated FDF03.

XX KW Human; type I transmembrane protein; immunoglobulin-like domain; FDF03;
 KW activated monocyte; YE01; KTE03; control; development; differentiation;
 KW mammalian immune system; treatment; cancerous condition;
 KW degenerative condition; autoimmune response; transplantation rejection;
 KW graft versus host disease; inflammatory condition; detection; diagnosis;
 KW drug screening.

XX OS Homo sapiens.

XX PN WO9824906-A2.

XX PD 11-JUN-1998.

XX PF 05-DEC-1997; 97WO-US021101.

XX PR 06-DEC-1996; 96US-0032252P.

XX PR 09-DEC-1996; 96US-00762187.

XX PR 16-DEC-1996; 96US-0033181P.

XX PR 21-MAR-1997; 97US-0041279P.

XX PA (SCHE) SCHERING CORP.

XX PI Adema GJ, Mevaard L, Gorman DM, Mcclanahan TK, Zurawski SM;

XX PI Zurawski G, Lanier LL, Phillips JH;

XX DR WPI; 1998-333325/29.

XX DR N-PSDB; AAV38987.

XX PT New isolated activated monocyte cell gene(s) - used to develop products
 PT for treating e.g. cancer, degenerative conditions, autoimmune responses,
 PT transplant rejection or inflammatory conditions.

XX PS Claim 1; Page 60-61; 104pp; English.

XX CC The present sequence represents a human protein, FDF03, which is a type I
 CC transmembrane protein comprising an extracellular portion characterised
 CC by immunoglobulin-like domains, indicating that the protein is a receptor
 CC member of the immunoglobulin superfamily. The FDF03 gene is found in
 CC activated monocytes. The specification also describes other proteins
 CC encoded by activated monocytes, which are designated YE01 and KTE03. The
 CC genes function in controlling development, differentiation, and/or
 CC physiology of the mammalian immune system. The products can be used for
 CC treating abnormal proliferation, regeneration, degeneration or atrophy.
 CC They can be used for treating e.g. cancerous conditions, degenerative
 CC conditions, autoimmune responses, transplantation rejection, graft versus
 CC host disease, or inflammatory conditions. The products can also be used
 CC for detection, diagnosis and drug screening

XX SQ Sequence 303 AA;

Query Match 87.9%; Score 821; DB 2; Length 303;
 Best Local Similarity 96.9%; Pred. No. 1.5e-69;
 Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRPLLLPPLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60

Db 1 MGRPLLLPPLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60

Qy 61 LATAPDVRIWRGHFHGQSFYSTRPPSIHKDYVNRFLNWTGQSGFLRISNLOKQDQ 120

Db 61 LATAPDVRIWRGHFHGQSFYSTRPPSIHKDYVNRFLNWTGQSGFLRISNLOKQDQ 120

Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTQ 159

Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQAVTTTQR 159

RESULT 3

AAW07443

ID AAW07443 standard; protein; 303 AA.

XX AC AAW07443;

XX DT 20-OCT-2000 (first entry)

XX DE A human monocyte-derived protein FDF03.

XX KW Human; monocyte-derived protein; FDF03; FDF03deltaTM; FDF03-S1;
 KW FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
 KW tissue rejection; inflammation; infection.

XX OS Homo sapiens.

XX PH Location/Qualifiers

FT Peptide 1..19 /note= "signal peptide"

FT Protein 20..303 /note= "mature protein"

XX WO2000040721-A1.

XX PD 13-JUL-2000.

XX PF 29-DEC-1999; 99WO-US030004.

XX PR 31-DEC-1998; 98US-00223919.

XX PR 31-DEC-1998; 98US-00224604.

XX PA (SCHE) SCHERING CORP.

XX PI Bates E, Fournier N, Chaulus L, Garrone P;

XX WPI; 2000-465984/40.

XX DR N-PSDB; AAA58814.

XX PT Novel monocyte-derived polypeptides and polynucleotides, used to diagnose

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:08 ; Search time 12.2093 Seconds
(without alignments)
1379.107 Million cell updates/sec

Title: US-10-780-043-8
Perfect score: 934
Sequence: 1 MCRPLLLLPLPLPPAPFLQ.....KTQRSHWRISGMKDIQIPS 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	10.9	572	2 B46529	Ig Y heavy chain (
2	101.5	10.9	1694	2 S50065	sialoadhesin - mou
3	101	10.8	118	2 E27889	Ig heavy chain V r
4	100.5	10.8	151	2 I46626	rearranged T-cell
5	97	10.4	142	2 A28344	VpreB protein prec
6	97	10.4	392	2 B44194	poliovirus recepto
7	97	10.4	417	2 A44194	Ig lambda chain V-
8	96.5	10.3	110	2 S57442	Ig lambda chain -
9	96	10.3	235	2 S25758	VpreB protein prec
10	95.5	10.2	142	2 B28344	Ig light chain V r
11	94.5	10.1	132	2 A52410	T-cell receptor de
12	93.5	10.0	131	2 S36301	Ig lambda chain pr
13	93.5	10.0	132	2 PL0114	Ig lambda chain pr
14	93.5	10.0	132	2 S04937	Ig lambda chain V-
15	93.5	10.0	136	2 S16848	Ig heavy chain V r
16	93	10.0	119	2 D27889	Ig heavy chain V r
17	93	10.0	132	2 I71935	MHC class II I-A-A
18	93	10.0	142	2 S36316	T-cell receptor de
19	93	10.0	403	2 I52590	m3-B isoform - mo
20	92.5	9.9	111	1 L2HUBH	Ig lambda chain V-
21	92	9.9	125	2 A31493	Ig light chain pre
22	92	9.9	773	1 ORRBG	secretory componen
23	91.5	9.8	137	2 S36311	T-cell receptor de
24	91.5	9.8	226	2 A46477	membrane-bound inm
25	91	9.7	112	2 S31515	Ig lambda chain V
26	91	9.7	113	1 L1CHV	Ig lambda chain pr
27	91	9.7	145	2 S36299	T-cell receptor de
28	90.5	9.7	118	2 S04519	Ig lambda chain pr
29	90.5	9.7	882	2 I38912	receptor tyrosine

antibody light cha
Ig lambda chain V-
T-cell receptor de
Ig lambda chain pr
T-cell receptor de
T-cell receptor de
poliovirus recepto
poliovirus recepto
proteoglycan core
Ig lambda chain -
Ig kappa chain V r
rearranged T-cell
Ig heavy chain pre
Ig light chain var
Ig lambda chain -
Ig lambda chain V-

ALIGNMENTS

RESULT 1

B46529
Ig Y heavy chain (7.8S) - duck
N:Alternate names: Ig gamma chain (7.8S)
C:Species: Anas platyrhynchos (domestic duck)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B46529; S20759
R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J. Immunol. 149, 2627-2633, 1992
A:Title: Structural relationship between the two IGY of the duck, Anas platyrhynchos: m
A:Reference number: A46529; MUID:93017865; PMID:1401901
A:Accession: B46529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-572 <MAG>
A:Cross-references: UNIPARC:UPI0000116038; EMBL:X65219; NID:G62442; PIDN:CAA46322.1; PFI
A:Experimental source: spleen
A:Note: sequence extracted from NCBI backbone (NCBIP:116127)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:37-120/Domain: immunoglobulin homology <IMM>

Query Match 10.9%; Score 102; DB 2; Length 572;

Best Local Similarity 24.7%; Pred. No. 0.13;

Matches 40; Conservative 29; Mismatches 57; Indels 36; Gaps 8;

QY 5 LLLPLLLPLPPAFLOPSGSTGSPSYLYGVTPQKHLASMGGSVEI-----PFSFY 57

Db LLLAAVPGURAAATLDESGG-----GLVSP-----GGSLTVCKSGGFTFSYG 55

QY 58 PWELATAPDVRISWRRG--HFHGQSFYSTRPSPSIHKDYVNRFLNWTGQKSGFLRISNL 115

Db VSVWQAFQKGLWAGITDSGSTYYA---PAVK---GRFTISRNNGQSTATLQMNSL 108

QY 116 QKQDSVFCRVREL--DTRSGRQWQSQIEGKLSITQGNPS 155

Db 109 KAEDTATYCAKGYGIRSDIDLWG--HGTEVAVSGSPT 148

RESULT 2

S50065

sialoadhesin - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S50065

R:Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Mi

EMBO J. 13, 4490-4503, 1994

A:Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells

A:Reference number: S50065; MUID:95009950; PMID:7925291

A:Accession: S50065

A:Status: preliminary

A:Molecule type: mRNA

A/Residues: 1-1694 <CRO>
A/Cross-references: UNIPROT:Q62230; UNIPARC:UPI0000028B74; EMBL:Z36293; NID:G557253; PID

Query Match 10.9%; Score 101.5; DB 2; Length 1694;
Best Local Similarity 24.0%; Pred. No. 0.54;
Matches 31; Conservative 26; Mismatches 57; Indels 15; Gaps 4;
QY 33 YGVTPKHLASMGSGSVIPSPFYYPWELATAPDVRIWRGHHFGQS-----FYSTRP 86
DB 21 WGVSPKRVQGLSGCLLIPISYPADVPVSGITAIW-----YDYSGKQVVIHSGDP 76
QY 87 PSIHKDYVNRFLNWTGQSGFLRISNLQKQDSVYFCRVELDTRSSGRQQWOSIEGTK 146
DB 77 KLVDKRPGRGRLAGMNDHKVNCNLLKDLKPEDSDTYNFRFEI----SDSNRLDVKGT 132
QY 147 LSITQGNPS 155
DB 133 VTVT--DPS 140

RESULT 3

E27889
Ig heavy chain V region (H18-8415) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: E27889
R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to a d
A/Reference number: A91043; MUID:86300658; PMID:2427335
A/Accession: E27889
A/Molecule type: DNA
A/Residues: 1-118 <CAT>
A/Cross-references: UNIPARC:UPI0000176869
A/Experimental source: strain Balb/c
A/Note: This sequence was determined from a hybridoma protein from the germline gene
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 10.8%; Score 101; DB 2; Length 118;
Best Local Similarity 24.8%; Pred. No. 0.023;
Matches 33; Conservative 25; Mismatches 35; Indels 40; Gaps 7;
QY 34 GVTQPKHLASMGSGSV-----IPSPFYYPWELATAPDVRIWRGHHFGQSFYSTRP 86
DB 10 GLVKP-----GSLKLSAASGITFSDYYMYVRYQTDPKRLW-----VATIT 52
QY 87 PSI---HKDYVNRFLNWTGQSGFLRISNLQKQDSVYFCRVELDTRSS-----GRQ 137
DB 53 DDINTYYSVDSVKGRFTISRDNAGNNYLQLSLKSEDTAMTC-----TRGSYYDYQMD 107
QY 138 QWQSTEGTKLSIT 150
DB 108 YWG--QGTSTVTS 118

RESULT 4

I46626
rearranged T-cell receptor delta-chain/ Vdelta.4-Ddelta.4 - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C/Accession: I46626
R/Jiang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A/Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A/Reference number: I46623; MUID:95363165; PMID:7636249
A/Accession: I46626
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-151 <YAN>
A/Cross-references: UNIPARC:UPI000011B2A5; GB:D49567; NID:G1041136; PIDN:BAA0511.1; PID

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 10.8%; Score 100.5; DB 2; Length 151;
Best Local Similarity 27.7%; Pred. No. 0.035;
Matches 39; Conservative 17; Mismatches 50; Indels 35; Gaps 4;
QY 6 LLPLLPALLPAPLQPSGSGSYLYGVTPQKHLASMGSGSVIEIPSFYYPWELATAP 65
DB 3 LSSLLMLFLTSVP-----SGSGVAQKVTDQPV-VSRQGEAVTLNCRSTSWNETI- 54
QY 66 DVRIWRGRGHFGQSFYSTRPPSIHKDYV-----NRLFLNWTGQSGFLRIS 113
DB 55 -----FWYKQPPSGEMTFLIYQYSASNAKGRVFINFQAKSLSLTIS 99
QY 114 NLQKQDSVYFCRVELDTRSS 134
DB 100 ALQLQDSATYFCALWVVVTMS 120

RESULT 5

A28344
VpreB protein precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C/Accession: A28344
R/Kudo, A.; Melchers, F.
EMBO J. 6, 2267-2272, 1987
A/Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be se
A/Reference number: A91077; MUID:88029315; PMID:3117530
A/Accession: A28344
A/Molecule type: DNA
A/Residues: 1-142 <KUD>
A/Cross-references: UNIPROT:P13372; UNIPARC:UPI0000003EE4; GB:X05556; GB:Y00079; NID:G55
A/Note: the authors translated the codon GAG for residue 110 as Gln
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/20-142/Product: VpreB1 protein #status predicted <MAT>

Query Match 10.4%; Score 97; DB 2; Length 142;
Best Local Similarity 25.5%; Pred. No. 0.068;
Matches 41; Conservative 22; Mismatches 40; Indels 58; Gaps 8;
QY 12 LLLPAPLQPSGSGSYLYGVTPQKHLASMGSGSVIEIPSFYYPWELATAPDVRIW 71
DB 7 LLMLLAVL-----TGCQPQM--VHQPPPLASSLGAT-----IRLSC 41
QY 72 RRGHHGQSFYST-----RPSIHKDYVNRFLNWTGQ-----KS 107
DB 42 TLSNDHNIGIYIYVYQQRPGHPPR----FLRYFHSKDKHQDPDIPRFSGSKDTTRNL 97
QY 108 GFLRISNLQKQDSVYFCRVELDTRSSGR--QQWQSTIEGTK 146
DB 98 GYLISELQPEDEAVYVYVYQVLRSGQEKRMEREW---EGEK 135

RESULT 6

B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C/Species: Cercopithecus aethiops (green monkey, grivet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: B44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no puta
A/Reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: B44194
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-392 <KOI>
A/Cross-references: UNIPROT:P32506; UNIPARC:UPI000002B1F7; GB:S48817
C/Superfamily: poliovirus receptor; immunoglobulin homology
F/259-314/Domain: immunoglobulin homology <IMM>

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 75.5168 Seconds
(without alignments)
1634.967 Million cell updates/sec

Title: US-10-780-043-8

Perfect score: 934

Sequence: 1 MGRPLLLPLLLPPAFLO.....KTQRSHMRISGMKDIQIPIS 175

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	821	87.9	303	Q9UKJ1_HUMAN	Q9ukj1 homo sapien
2	816	87.4	226	Q8NH11_HUMAN	Q8nh11 homo sapien
3	742.5	79.5	227	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
4	347	37.2	299	Q8BYA6_MOUSE	Q8bya6 mus musculus
5	121.5	13.0	633	Q5W434_BRARE	Q5w434 brachydanio
6	121.5	13.0	651	Q5W433_BRARE	Q5w433 brachydanio
7	109.5	11.7	233	Q8TBC9_HUMAN	Q8tbc9 homo sapien
8	103.5	11.1	235	Q6P2J1_HUMAN	Q6p2j1 homo sapien
9	102.5	11.0	149	Q69YF9_HUMAN	Q69yf9 homo sapien
10	102.5	11.0	271	Q9HBS0_HUMAN	Q9hbso homo sapien
11	102.5	11.0	400	Q4T054_TETNG	Q4t054 tetraodon n
12	101.5	10.9	1694	1 SN_MOUSE	Q62230 mus musculus
13	100.5	10.8	551	1 SIGL5_HUMAN	Q15389 homo sapien
14	100	10.7	236	Q6PIQ7_HUMAN	Q6piq7 homo sapien
15	100	10.7	325	Q501V7_BRARE	Q501v7 brachydanio
16	97	10.4	142	1 VPRI1_MOUSE	P13372 mus musculus
17	97	10.4	142	Q5W1K4_MOUSE	Q5w1k4 mus musculus
18	97	10.4	142	Q545E0_MOUSE	Q545e0 m 13 days e
19	97	10.4	417	1 FV5_CERAE	P32506 cercopithec
20	96	10.3	302	Q4T853_TETNG	Q4t853 tetraodon n
21	96	10.3	328	Q6ZMC9_HUMAN	Q6zmc9 homo sapien
22	96	10.3	394	Q6UXG0_HUMAN	Q6uxg0 homo sapien
23	95.5	10.2	142	1 VPRE2_MOUSE	P13373 mus musculus
24	95.5	10.2	479	Q7TMK4_MOUSE	Q7tmk4 mus musculus
25	95	10.2	360	1 HPLN3_HUMAN	Q96886 homo sapien
26	95	10.2	595	2 Q5W431_FUGRU	Q5w431 fugu rubrip
27	95	10.2	630	2 Q5W436_FUGRU	Q5w436 fugu rubrip
28	95	10.2	648	2 Q5W435_FUGRU	Q5w435 fugu rubrip
29	95	10.2	1709	1 SN_HUMAN	Q9bzz2 homo sapien
30	95	10.2	1730	2 Q7YRQ7_PIG	Q7yrq7 sus scrofa
31	94.5	10.1	235	2 Q6FUG0_HUMAN	Q6pfug0 homo sapien

32	94.5	10.1	358	2	Q7QAJ4_ANOGA	Q7qaj4 anopheles g
33	93.5	10.0	235	2	Q99M11_MOUSE	Q99m11 mus musculu
34	93.5	10.0	255	2	Q6KB05_MOUSE	Q6kb05 mus musculu
35	93.5	10.0	1035	2	Q6Q179_RAT	Q6q179 rattus norv
36	93	10.0	269	2	Q95KP8_PONPY	Q95kp8 pongo pygma
37	93	10.0	403	1	CD33_MOUSE	Q63994 mus musculu
38	92.5	9.9	111	1	LV2C_HUMAN	P01706 homo sapien
39	92.5	9.9	172	2	Q4TBU3_TETNG	Q4tbu3 tetraodon n
40	92.5	9.9	233	2	Q6GNH3_XENLA	Q6gnh3 xenopus lae
41	92	9.9	773	1	P1GR_RABIT	P01832 corytolagus
42	92	9.9	1032	1	CNT1A_BRARE	Q8axz4 brachydanio
43	91.5	9.8	226	1	CD79A_HUMAN	P11912 homo sapien
44	91	9.7	113	1	LV1_CHICK	P04210 gallus gall
45	91	9.7	236	2	Q6P5S3_HUMAN	Q6p5s3 homo sapien

ALIGNMENTS

RESULT 1
Q9UKJ1_HUMAN PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2004 (Tremblrel. 26, Last annotation update)
DE Inhibitory receptor PILRALpha.
GN Name=PILRA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is paired with the truncated counterpart PILRBeta.";
RL J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161080; AAD52964.1; -; mRNA.
DR Ensembl; ENSG00000085514; Homo sapiens.
DR HGNC; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; F:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PSF0835; IG_LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 303 AA; 33878 MW; 0410ADFC7E80928B CRC64;

Query Match 87.9%; Score 821; DB 2; Length 303;
Best Local Similarity 96.9%; Pred. No. 1.5e-69;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MGRPLLLPLLLPPAFLOPSGSGPSYLYGVTOPKHLASMGSGVEIPFSFYYPWE 60
DB 1 MGRPLLLPLLLPPAFLOPSGSGPSYLYGVTOPKHLASMGSGVEIPFSFYYPWE 60
QY 61 LATAPDVRIWMRRGHFGHGSFYSTRPPSHKHQYVNRFLNWTGQKSGFLRISLNQKQDQ 120
DB 61 LATAPDVRIWMRRGHFGHGSFYSTRPPSHKHQYVNRFLNWTGQKSGFLRISLNQKQDQ 120
QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTQR 159
DB 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTQR 159

RESULT 2
Q8NH11_HUMAN

ID Q8NH11 HUMAN PRELIMINARY; PRT; 226 AA.
 AC Q8NH11;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE PILRA protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lung;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blackley R.W., Truchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gough J.J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.B.,
 RA Scherch A., Schein J.R., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017812; AAI17812.1; -; mRNA.
 DR InterPro; IPR003599; IG.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 226 AA; 25479 MW; 539818197733A30 CRC64;

 Query Match 87.4%; Score 816; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 3e-69;
 Matches 152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPQKLSASMGSGVEIPFSPYFWE 60
 Db 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPQKLSASMGSGVEIPFSPYFWE 60

 Qy 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYNNRLFLNWTGQKSGFLRISNLQKODQ 120
 Db 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYNNRLFLNWTGQKSGFLRISNLQKODQ 120

 Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQG 152
 Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQG 152

 RESULT 3
 ID Q9UKJ0 HUMAN PRELIMINARY; PRT; 227 AA.
 AC Q9UKJ0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Activating receptor PILRbeta (Hypothetical protein DKFP24340079).

GN Name=DKFP24340079;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Testis;
 RC The German CDNA Consortium;
 RG Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (GEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- INTERACTION:
 CC O95870:BATS; NDBxp=1; IntAct=EBI-347958, EBI-348517;
 CC EMBL; AF161081; AAD52365.1; -; mRNA.
 DR EMBL; AL834336; CAH10711.1; -; mRNA.
 DR IntAct; O9UKJ0; -;
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; NAS.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 1.
 KW Hypothetical protein; Immunoglobulin domain; Receptor.
 SQ SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7EF09 CRC64;

 Query Match 79.5%; Score 742.5; DB 2; Length 227;
 Best Local Similarity 81.7%; Pred. No. 3e-62;
 Matches 143; Conservative 9; Mismatches 12; Indels 11; Gaps 2;

 Qy 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPQKLSASMGSGVEIPFSPYFWE 60
 Db 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPQKLSASMGSGVEIPFSPYFWE 60

 Qy 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYNNRLFLNWTGQKSGFLRISNLQKODQ 120
 Db 61 LATAPDVRIWRGRGHFGQSFYSTRPSIHKDYNNRLFLNWTGQKSGFLRISNLQKODQ 120

 Qy 121 SVYFCRVELDTSSGRQWQSIETGKLSITQG-----NPSKTQSRSHRISGMK 168
 Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQAVTTTTPRPST----TTIAGLR 171

 RESULT 4
 ID Q8BYA6 MOUSE PRELIMINARY; PRT; 299 AA.
 AC Q8BYA6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
 DE library, clone:A630007P20 product:weakly similar to INHIBITORY
 DE RECEPTOR PILRALPHA.
 GN Name=Pilra; Synonym=AV021745;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Thymus;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 18.2386 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-8
Perfect score: 934
Sequence: 1 MGRPPLLLPPLPPAPLQ.....KTQRSHMRISGMKDKIQIPS 175

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgm2_6/ptodata/1/1aa/5 COMB.pep.*
2: /cgm2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgm2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgm2_6/ptodata/1/1aa/PCITUS COMB.pep.*
5: /cgm2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgm2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934	100.0	175	2	US-09-869-388-8
2	821	87.9	303	2	US-08-985-950-2
3	821	87.9	303	2	US-09-546-043-2
4	821	87.9	303	2	US-09-869-388-2
5	816	87.4	230	2	US-09-869-388-4
6	757.5	81.1	226	2	US-09-869-388-10
7	743.5	79.6	238	2	US-09-149-476-485
8	742.5	79.5	227	2	US-09-869-388-6
9	517	55.4	101	2	US-09-149-476-754
10	222	23.8	99	2	US-08-985-950-4
11	222	23.8	99	2	US-09-546-043-4
12	109.5	11.7	244	2	US-08-918-148-79
13	109.5	11.7	244	2	US-09-138-091A-77
14	100.5	10.8	551	2	US-08-896-537A-2
15	100	10.7	284	2	US-09-184-658-40
16	100	10.7	284	2	US-09-504-262D-40
17	98	10.5	355	2	US-08-875-811-57
18	97.5	10.4	104	2	US-10-083-424-40
19	97.5	10.4	553	1	US-08-661-052-16
20	97.5	10.4	553	2	US-09-188-082-16
21	97.5	10.4	553	2	US-09-364-088-16
22	97.5	10.4	553	2	US-09-102-716-16
23	95.5	10.2	421	2	US-08-759-628-5
24	95	10.2	143	1	US-08-345-321-8
25	95	10.2	360	2	US-09-907-794A-213
26	95	10.2	360	2	US-09-905-125A-213
27	95	10.2	360	2	US-09-902-775A-213

28 95 10.2 360 2 US-09-906-700-213 Sequence 213, App
29 95 10.2 360 2 US-09-903-603A-213 Sequence 213, App
30 95 10.2 360 2 US-09-904-920A-213 Sequence 213, App
31 95 10.2 360 2 US-09-905-064-213 Sequence 213, App
32 95 10.2 360 2 US-09-905-381A-213 Sequence 213, App
33 95 10.2 360 2 US-09-906-618-213 Sequence 213, App
34 95 10.2 360 2 US-09-906-646-213 Sequence 213, App
35 95 10.2 360 2 US-09-904-462-213 Sequence 213, App
36 95 10.2 360 2 US-09-903-736A-213 Sequence 213, App
37 95 10.2 360 2 US-09-906-722A-213 Sequence 213, App
38 95 10.2 1709 2 US-09-949-016-10503 Sequence 10503, A
39 94.5 10.1 126 2 US-08-751-359-11 Sequence 11, Appl
40 94.5 10.1 126 2 US-08-907-146-11 Sequence 11, Appl
41 94.5 10.1 262 2 US-09-069-821-4 Sequence 4, Appl
42 94.5 10.1 262 2 US-09-956-086-4 Sequence 4, Appl
43 94.5 10.1 262 2 US-09-956-087-4 Sequence 4, Appl
44 94.5 10.1 282 2 US-09-420-592A-7 Sequence 7, Appl
45 94.5 10.1 282 2 US-09-985-442-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-869-388-8
; Sequence 8, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-8

Query Match 100.0%; Score 934; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.4e-89;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGRPPLLLPPLPPAPLQPSGSGPSYLYGTQPKHLSASMGSGVEIPFSYPWE 60
DB 1 MGRPPLLLPPLPPAPLQPSGSGPSYLYGTQPKHLSASMGSGVEIPFSYPWE 60
QY 61 LATAPDVRIWRGHFGHGSFYSTRPPSIHKDYVNRFLNWTGKSGFLRISNLQKQDQ 120
DB 61 LATAPDVRIWRGHFGHGSFYSTRPPSIHKDYVNRFLNWTGKSGFLRISNLQKQDQ 120
QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTQRSHMRISGMKDKIQIPS 175
DB 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTQRSHMRISGMKDKIQIPS 175

RESULT 2
US-08-985-950-2
; Sequence 2, Application US/08985950
; Patent No. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto

STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-950-2

Query Match 87.9%; Score 821; DB 2; Length 303;
Best Local Similarity 96.9%; Pred. No. 1.8e-77;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
Db 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
Qy 61 LATAPDVRIWRRGHGHGQSFYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKODQ 120
Db 61 LATAPDVRIWRRGHGHGQSFYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKODQ 120
Qy 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTOR 159
Db 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTQR 159

RESULT 3
US-09-546-049-2
Sequence 2, Application US/09546049
Patent No. 6479638
GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
Meygaard, Linde
Gorman, Daniel M.
McClanahan, Terrill K.
Zurawski, Sandra M.
Zurawski, Gerard
Kanier, Lewis L.
Phillips Jr., Joseph H.
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
Related Reagents
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue,
CITY: Palo Alto

STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,049
FILING DATE: 10-APR-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-546-049-2

Query Match 87.9%; Score 821; DB 2; Length 303;
Best Local Similarity 96.9%; Pred. No. 1.8e-77;
Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
Db 1 MGRPLLLPLLLPPAPLPQSGTSGSPSYLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
Qy 61 LATAPDVRIWRRGHGHGQSFYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKODQ 120
Db 61 LATAPDVRIWRRGHGHGQSFYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKODQ 120
Qy 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTOR 159
Db 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTQR 159

RESULT 4
US-09-869-388-2
Sequence 2, Application US/09869388
Patent No. 6774214
GENERAL INFORMATION:
APPLICANT: Bates, Elizabeth
APPLICANT: Fournier, Nathalie
APPLICANT: Chalus, Lionel
APPLICANT: Garrone, Pierre
TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
FILE REFERENCE: SF0977X
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 2
LENGTH: 303
TYPE: PRT
ORGANISM: homo sapiens
US-09-869-388-2

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:40:10 ; Search time 59.5392 Seconds
(without alignments)
1228.101 Million cell updates/sec

Title: US-10-780-043-8

Perfect score: 934

Sequence: 1 MGRPLLPLPLPLPPAPLQ.....KTRSHWRISGMKDIQIPS 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	821	87.9	303	3	US-09-774-381-58
3	821	87.9	303	4	US-10-290-631-2
4	821	87.9	303	4	US-10-780-043-2
5	821	87.9	303	4	US-10-777-524-2
6	821	87.9	303	5	US-10-777-521-2
7	816	87.4	230	4	US-10-309-290-110
8	816	87.4	230	4	US-10-780-043-4
9	809.5	86.7	1012	5	US-10-450-763-30868
10	809.5	86.7	1012	5	US-10-450-763-33210
11	809.5	86.7	1012	5	US-10-450-763-47228
12	809.5	86.7	1012	5	US-10-450-763-51762
13	757.5	81.1	226	3	US-09-745-763-106
14	757.5	81.1	226	3	US-09-774-381-44
15	757.5	81.1	226	3	US-10-780-043-10
16	743.5	79.6	238	3	US-09-809-391-485
17	743.5	79.6	238	3	US-09-882-171-485
18	743.5	79.6	238	4	US-10-164-861-485
19	742.5	79.5	227	4	US-10-262-445-128
20	742.5	79.5	227	4	US-10-780-043-6
21	742.5	79.5	227	5	US-10-820-474A-7
22	742.5	79.5	291	3	US-09-935-390A-21
23	742.5	79.5	326	4	US-10-276-774-2380
24	655	70.1	206	4	US-10-309-290-112
25	517	55.4	101	3	US-09-809-391-754
26	517	55.4	101	3	US-09-882-171-754
27	517	55.4	101	4	US-10-164-861-754

28 342.5 35.7 224 3 US-09-866-050A-711 Sequence 711, App
29 222 23.8 99 4 US-10-290-631-4 Sequence 4, Appli
30 222 23.8 99 4 US-10-777-524-4 Sequence 4, Appli
31 222 23.8 99 5 US-10-777-521-4 Sequence 4, Appli
32 120.5 12.9 124 5 US-10-788-625-92 Sequence 92, Appl
33 116.5 12.5 253 4 US-10-479-670-184 Sequence 184, App
34 115.5 12.4 247 4 US-10-479-670-158 Sequence 158, App
35 114.5 12.3 252 4 US-10-479-670-168 Sequence 168, App
36 114.5 12.3 253 4 US-10-479-670-174 Sequence 174, App
37 114.5 12.3 253 4 US-10-779-461-18 Sequence 18, Appl
38 110.5 11.8 246 3 US-09-880-748-2077 Sequence 2077, Ap
39 110.5 11.8 246 3 US-09-880-748-2079 Sequence 2079, Ap
40 110.5 11.8 246 4 US-10-293-418-2077 Sequence 2077, Ap
41 110.5 11.8 246 4 US-10-293-418-2079 Sequence 2079, Ap
42 109.5 11.7 244 5 US-10-778-394-77 Sequence 77, Appl
43 109.5 11.7 245 4 US-10-139-785-48 Sequence 48, Appl
44 109.5 11.7 245 5 US-10-986-046-48 Sequence 48, Appl
45 109.5 11.7 245 5 US-10-986-047-48 Sequence 48, Appl

ALIGNMENTS

RESULT 1

US-10-780-043-8
; Sequence 8, Application US/10780043
; Publication No. US20040137506A1
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METH
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/10/780,043
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/869,388
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-780-043-8

Query Match 100.0%; Score 934; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 5.5e-81; Indels 0; Gaps 0;
Matches 175; Conservative 0; Mismatches 0;
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Db 1 MGRPLLPLPLPLPPAPLQPSGSGSYLYGVTPQKHLASMGSGSYVEIPFSYYPWE 60
QY 61 LATAPDVRIWRGRHFGHQSFSYTPPSIHKDYVRLFLNWTGQKSGFLRISNLOKQDQ 120
Db 61 LATAPDVRIWRGRHFGHQSFSYTPPSIHKDYVRLFLNWTGQKSGFLRISNLOKQDQ 120
QY 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTSRSHMRISGMKDKIQIPS 175
Db 121 SVYFCRVELDTSSGRQWQSIETGKLSITQGNPSKTSRSHMRISGMKDKIQIPS 175

RESULT 2

US-09-774-381-58
; Sequence 58, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; APPLICANT: Gearring, David P.
; TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES

; TITLE OF INVENTION: AND USES THEREFOR
 ; FILE REFERENCE: MNI-107CP2
 ; CURRENT APPLICATION NUMBER: US/09/774,381
 ; CURRENT FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: 08/941,354
 ; PRIOR FILING DATE: 1999-09-30
 ; PRIOR APPLICATION NUMBER: 09/010,674
 ; PRIOR FILING DATE: 1998-01-22
 ; PRIOR APPLICATION NUMBER: 60/061,149
 ; PRIOR FILING DATE: 1997-10-06
 ; PRIOR APPLICATION NUMBER: 09/014,347
 ; PRIOR FILING DATE: 1998-01-27
 ; PRIOR APPLICATION NUMBER: 60/061,159
 ; PRIOR FILING DATE: 1997-10-06
 ; PRIOR APPLICATION NUMBER: 09/474,151
 ; PRIOR FILING DATE: 2000-12-21
 ; PRIOR APPLICATION NUMBER: 09/004,206
 ; PRIOR FILING DATE: 1998-01-08
 ; PRIOR APPLICATION NUMBER: 60/061,143
 ; PRIOR FILING DATE: 1997-10-06
 ; PRIOR APPLICATION NUMBER: 09/483,414
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 09/213,571
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: 08/994,890
 ; PRIOR FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 59
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 58
 ; LENGTH: 303
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-774-381-58

Query Match 87.9%; Score 821; DB 3; Length 303;
 Best Local Similarity 96.9%; Pred. No. 6.5e-70;
 Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MGRLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Db 1 MGRLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Qy 61 LATAPDVRIWRGHFGQSFYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120
 Db 61 LATAPDVRIWRGHFGQSFYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120
 Qy 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTOR 159
 Db 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTQOR 159

RESULT 3
 US-10-230-631-2
 ; Sequence 2, Application US/102990631
 ; Publication No. US20030105303A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Adema, Gosse Jan
 ; Meyard, Linde
 ; Gorman, Daniel M.
 ; McClanahan, Terrill K.
 ; Zurawski, Sandra M.
 ; Zurawski, Gerard
 ; Lanier, Lewis L.
 ; Phillips Jr., Joseph H.
 ; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA

; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/290,631
 ; FILING DATE: 08-No. US20030105303A1-2002.
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/985,950
 ; FILING DATE: 05-DEC-1997
 ; APPLICATION NUMBER: US 60/041,279
 ; FILING DATE: 21-MARCH-1997
 ; APPLICATION NUMBER: US 60/033,181
 ; FILING DATE: 16-DEC-1996
 ; APPLICATION NUMBER: US 60/032,252
 ; FILING DATE: 06-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; REFERENCE/DOCKET NUMBER: DX0670K
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 852-9196
 ; TELEFAX: (650) 496-1204
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 303 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-10-290-631-2

Query Match 87.9%; Score 821; DB 4; Length 303;
 Best Local Similarity 96.9%; Pred. No. 6.5e-70;
 Matches 154; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 MGRLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 Db 1 MGRLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
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 Db 61 LATAPDVRIWRGHFGQSFYSTRPSIHKDYVNRFLNWTGQKSGFLRISNLQKQDQ 120
 Qy 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQGNPSKTOR 159
 Db 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTQOR 159

RESULT 4
 US-10-780-043-2
 ; Sequence 2, Application US/10780043
 ; Publication No. US20040137506A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bates, Elizabeth
 ; APPLICANT: Fournier, Nathalie
 ; APPLICANT: Chalus, Lionel
 ; APPLICANT: Garone, Pierre
 ; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
 ; FILE REFERENCE: SF0977X
 ; CURRENT APPLICATION NUMBER: US/10/780,043
 ; CURRENT FILING DATE: 2004-02-17
 ; PRIOR APPLICATION NUMBER: US/09/869,388
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: IBM PC compatible
 ; SEQ ID NO 2
 ; LENGTH: 303
 ; TYPE: PRT
 ; ORGANISM: homo sapiens

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2005, 20:41:30 ; Search time 3.31611 Seconds
(without alignments)
376.418 Million cell updates/sec

Title: US-10-780-043-8

Perfect score: 934

Sequence: 1 MGRPLLLPLPLPPAPLQ.....KIQSHWRISGMKDKIQIPS 175

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	113	12.1	327	US-10-512-184-62	Sequence 62, Appl
3	113	12.1	327	US-10-512-184-64	Sequence 64, Appl
4	113	12.1	328	US-10-512-184-63	Sequence 63, Appl
5	113	12.1	576	US-10-512-184-65	Sequence 65, Appl
6	113	12.1	625	US-10-512-184-47	Sequence 47, Appl
7	110.5	11.8	246	US-11-054-515-2077	Sequence 2077, Ap
8	110.5	11.8	246	US-11-054-515-2079	Sequence 2079, Ap
9	108.5	11.6	256	US-11-054-515-907	Sequence 907, Ap
10	106.5	11.4	250	US-10-512-184-27	Sequence 27, Appl
11	106	11.3	250	US-11-054-515-1319	Sequence 1319, Ap
12	106	11.3	258	US-11-054-515-1841	Sequence 1841, Ap
13	103	11.0	251	US-11-054-515-1827	Sequence 1827, Ap
14	102.5	11.0	250	US-11-054-515-3247	Sequence 3247, Ap
15	102.5	11.0	252	US-11-054-515-1021	Sequence 1021, Ap
16	102	10.9	245	US-11-054-515-1864	Sequence 1864, Ap
17	102	10.9	247	US-11-054-515-1751	Sequence 1751, Ap
18	102	10.9	250	US-11-054-515-837	Sequence 837, App
19	102	10.9	250	US-11-054-515-867	Sequence 867, App
20	102	10.9	250	US-11-054-515-1313	Sequence 1313, Ap
21	101.5	10.9	252	US-11-054-515-1787	Sequence 1787, Ap
22	100.5	10.8	242	US-11-054-515-1884	Sequence 1884, Ap
23	100.5	10.8	249	US-11-054-515-540	Sequence 540, App
24	100.5	10.8	254	US-11-054-515-1525	Sequence 1525, Ap
25	100.5	10.8	256	US-11-054-515-2080	Sequence 2080, Ap

ALIGNMENTS

RESULT 1

US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi

; FILE REFERENCE: 3581.01US01

; CURRENT APPLICATION NUMBER: US/10/512,184

; CURRENT FILING DATE: 2004-10-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 26

; LENGTH: 258

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURES:

; OTHER INFORMATION: Description of Artificial Sequence: scFv CWP2

; OTHER INFORMATION: with specificity against Fusarium spp.; originates

; OTHER INFORMATION: from Gallus gallus.

US-10-512-184-26

Query Match 12.1%; Score 113; DB 6; Length 258;
Best Local Similarity 31.5%; Pred. NO. 0.00048;
Matches 45; Conservative 18; Mismatches 44; Indels 36; Gaps 9;
QY 23 GSTSGPSYLVGVTPKHLASMGGSVIPPS---FYYPW----ELATAPDVRIWRCH 75
DB 141 GSKGAP-----LTQPSVSANLGTVEITCSGGYRGWFOOKSPGSAFVTIYM----192
QY 76 FHQGSFYTRPPSIHKDVVNLFLNWTGQKSG---FLRISNLQKQDSVYFCRVELDTR 132
DB 193 ---DDDSANRPSNIPSRP-----SGTSGSTATLTITGVQADDEAVYFGSY--DR 238

RESULT 2

US-10-512-184-62

; Sequence 62, Application US/10512184

; Publication No. US20050244901A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2005, 20:41:30 ; Search time 4.30146 Seconds
(without alignments)
376.418 Million cell updates/sec

Title: US-10-780-043-6

Perfect score: 1192

Sequence: 1 MGRPRLPLLLQLPPAFQ.....CLLLWRRKGRAPSSDP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	9.1	250	6	US-10-512-184-27
2	106.5	8.9	247	7	US-11-054-515-1294
3	106	8.9	250	7	US-11-054-515-2073
4	103.5	8.7	247	7	US-11-054-515-1328
5	103	8.6	250	7	US-11-054-515-2095
6	102.5	8.6	249	7	US-11-054-515-1030
7	102.5	8.6	252	7	US-11-054-515-897
8	102.5	8.6	252	7	US-11-054-515-1016
9	102.5	8.6	252	7	US-11-054-515-1131
10	102.5	8.6	252	7	US-11-054-515-1135
11	102.5	8.6	252	7	US-11-054-515-1163
12	102.5	8.6	253	7	US-11-054-515-902
13	102	8.6	258	6	US-10-512-184-26
14	102	8.6	327	6	US-10-512-184-62
15	102	8.6	327	6	US-10-512-184-64
16	102	8.6	328	6	US-10-512-184-63
17	102	8.6	576	6	US-10-512-184-65
18	102	8.6	625	6	US-10-512-184-47
19	101.5	8.5	256	7	US-11-054-515-907
20	100.5	8.4	254	7	US-11-054-515-1893
21	99.5	8.3	241	7	US-11-054-515-1911
22	99.5	8.3	250	7	US-11-054-515-1319
23	99	8.3	252	7	US-11-054-515-1549
24	98.5	8.3	246	7	US-11-054-515-2079
25	98.5	8.3	252	7	US-11-054-515-1145

ALIGNMENTS

RESULT 1

US-10-512-184-27

; Sequence 27, Application US/10512184

; Publication No. US2005024901A1

; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.v.

; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant

; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease

; TITLE OF INVENTION: resistance against fungi

; FILE REFERENCE: 3581.01US01

; CURRENT APPLICATION NUMBER: US/10/512,184

; CURRENT FILING DATE: 2004-10-22

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 27

; LENGTH: 250

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: scFv SGB3 with

; OTHER INFORMATION: specificity against Fusarium spp.; originates from

; OTHER INFORMATION: Gallus gallus.

US-10-512-184-27

Query Match 9.1%; Score 109; DB 6; Length 250;

Best Local Similarity 29.5%; Pred. No. 0.0014;

Matches 33; Conservative 19; Mismatches 34; Indels 26; Gaps 5;

QY 21 PG-GSTGSPSYLYGVCTOPKHLASMGSGSVETPPFSFYYPWELAIYVNVRISSHRGHFHQ 79

DB 134 PEGEGTKGAPA---LTQPSVSANLGTGVTIKTC-----GSTAHYSWHQKSPGS 180

QY 80 -----SFVSTRPPIHDKYVNRFLFNWTEGSEFLRISNLRKEDQSVYFC 125

DB 181 APVTLLISFNQRPSPDPSRF-----SGSKSGSTGLITGVRAEDAVYVC 226

RESULT 2

US-11-054-515-1294

; Sequence 1294, Application US/11054515

; Publication No. US2005025532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

```
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1294
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1294

Query Match      8.9%  Score 106.5; DB 7; Length 247;
Best Local Similarity 23.7%; Pred. No. 0.0023;
Matches 52; Conservative 26; Mismatches 78; Indels 63; Gaps 8;

Qy 19 LQCGSTGSGPSYLYGVTPQKHLGASMGSGVEIPFSFYPMWELAI VNVNRISM----- 71
Db 12 VKPGGSL-----RLCAASG---FTFSDYY-----MSWIRQAPGK 43

Qy 72 ---RRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEGQSGFLRISNLRKEDQSYVFC-RV 127
Db 44 GLERVSYSISSSSYIYADVSK-----GRFTISRDNAKNSLYLQNSLRAEDTAVYICARV 99

Qy 128 ELDTFRSGRQLOQSIKGTKLITQAVTTTWTWRSSTTTIA---GLRVTESKGHSWSHL 184
Db 100 KRQ-----ILTYGVGMDVWGKGTVTTVSSGGGGGGGGGGSSSEL 142

Qy 185 SLDTAIRVALAVALKTVILGLLCLLLWRRRRKGSRAP 223
Db 143 TODPAVSALQGVTRITCQGSLSRYASWYQRPQGP 181

RESULT 3
US-11-054-515-2073
/ Sequence 2073, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1328
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1328

Query Match      8.7%  Score 103.5; DB 7; Length 247;
Best Local Similarity 24.5%; Pred. No. 0.0045;
Matches 47; Conservative 28; Mismatches 78; Indels 39; Gaps 8;

Qy 46 GGSVEI-----PFSFYPMWELAI VNVNRISM-----RRGHFGQSFYSTRPPSIHKDYV 94
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/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2073
/ LENGTH: 250
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2073

Query Match      8.9%  Score 106; DB 7; Length 250;
Best Local Similarity 25.8%; Pred. No. 0.0027;
Matches 46; Conservative 24; Mismatches 58; Indels 50; Gaps 9;

Qy 46 GGSVEI-----PFSFYPMWELAI VNVNRISMRRGHF---HGQSFYSTRPPSIHKDYV 95
Db 15 GSSVKVSKASGGTFFSSYALSWRQAPGQGLEW-MGIFIFIGTEYYAER-----PQG 66

Qy 96 RLFLNWTGQSGFLRISNLRKEDQSYVFC-RVELDTRRSGRQLOQSIKGTKLIT--- 150
Db 67 RVTITADESTNTAYLDLSLSRSEDATVYICARVDYTDYEMGAFDLWG-QGTLVTVSSGGG 125

Qy 151 -----QAVTTTTTTPSPSTTTIAGLRVTES-----KGHSWSHL 186
Db 126 GSGGGGGGGGSAQAVLT-----QPSVSGAPGQRTVITCTGSSSNTGAGYDVHWYQQL 179

RESULT 4
US-11-054-515-1328
/ Sequence 1328, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1328
/ LENGTH: 247
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1328

Query Match      8.7%  Score 103.5; DB 7; Length 247;
Best Local Similarity 24.5%; Pred. No. 0.0045;
Matches 47; Conservative 28; Mismatches 78; Indels 39; Gaps 8;

Qy 46 GGSVEI-----PFSFYPMWELAI VNVNRISM-----RRGHFGQSFYSTRPPSIHKDYV 94
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2005, 20:40:10 ; Search time 77.2308 Seconds
(without alignments)
1228.101 Million cell updates/sec

Title: US-10-780-043-6

Perfect score: 1192

Sequence: 1 MGRPLLLPLLLLLQPPAFLO.....CLLLWRRRKGRAPSSDP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1192	100.0	227	4	US-10-262-445-128: Sequence 128, App
2	1192	100.0	227	4	US-10-780-043-6: Sequence 6, Appli
3	1192	100.0	227	5	US-10-820-473-7: Sequence 7, Appli
4	1192	100.0	291	3	US-69-945-390A-3: Sequence 21, Appl
5	1192	100.0	326	4	US-10-276-774-2380: Sequence 2380, Ap
6	1163.5	97.6	226	3	US-09-774-381-44: Sequence 44, Appl
7	1163.5	97.6	226	4	US-10-780-043-10: Sequence 10, Appl
8	1157.5	97.1	226	3	US-09-745-763-106: Sequence 106, App
9	1069	89.7	238	3	US-09-809-391-485: Sequence 485, App
10	1069	89.7	238	3	US-09-882-171-485: Sequence 485, App
11	1069	89.7	238	4	US-10-164-861-485: Sequence 485, App
12	958	80.4	303	3	US-09-774-381-58: Sequence 58, Appl
13	958	80.4	303	4	US-10-290-631-2: Sequence 2, Appli
14	958	80.4	303	4	US-10-780-043-2: Sequence 2, Appli
15	958	80.4	303	4	US-10-777-524-2: Sequence 2, Appli
16	958	80.4	303	5	US-10-777-521-2: Sequence 2, Appli
17	752	63.1	1012	5	US-10-450-763-30868: Sequence 30868, A
18	752	63.1	1012	5	US-10-450-763-33210: Sequence 33210, A
19	752	63.1	1012	5	US-10-450-763-47228: Sequence 47228, A
20	752	63.1	1012	5	US-10-450-763-51762: Sequence 51762, A
21	744	62.4	230	4	US-10-309-290-110: Sequence 110, App
22	744	62.4	230	4	US-10-780-043-4: Sequence 4, Appli
23	742.5	62.3	175	4	US-10-780-043-8: Sequence 8, Appli
24	592	49.7	206	4	US-10-309-290-112: Sequence 112, App
25	532	44.6	101	3	US-09-809-391-754: Sequence 754, App
26	532	44.6	101	3	US-09-882-171-754: Sequence 754, App
27	532	44.6	101	4	US-10-164-861-754: Sequence 754, App

28	370	31.0	224	3	US-09-866-050A-711	Sequence 711, App
29	223	18.7	99	4	US-10-290-631-4	Sequence 4, Appli
30	223	18.7	99	4	US-10-777-524-4	Sequence 4, Appli
31	223	18.7	99	5	US-10-777-521-4	Sequence 4, Appli
32	122	10.2	257	4	US-10-270-073-8	Sequence 8, Appli
33	120.5	10.1	256	4	US-10-270-073-6	Sequence 6, Appli
34	116.5	9.8	124	5	US-10-788-625-92	Sequence 92, Appl
35	116.5	9.8	253	4	US-10-479-670-174	Sequence 174, App
36	114	9.6	261	4	US-10-270-071-18	Sequence 18, Appl
37	114	9.6	261	4	US-10-270-073-2	Sequence 2, Appli
38	114	9.6	261	4	US-10-328-190-6	Sequence 6, Appli
39	112	9.4	352	3	US-09-203-958A-2	Sequence 2, Appli
40	112	9.4	352	5	US-10-764-131-2	Sequence 2, Appli
41	111	9.3	246	3	US-09-909-567B-49	Sequence 49, Appl
42	111	9.3	252	4	US-10-479-670-168	Sequence 168, App
43	110.5	9.3	310	4	US-10-052-798-11	Sequence 11, Appl
44	110.5	9.3	310	4	US-10-288-917-11	Sequence 11, Appl
45	110.5	9.3	310	4	US-10-423-448-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-10-262-445-128

Sequence 128, Application US/10262445

Publication No. US20040014058A1

GENERAL INFORMATION:

APPLICANT: Alsbrook II, John

APPLICANT: Burgess, Catherine

APPLICANT: Catterton, Elina

APPLICANT: Chant, John

APPLICANT: Chaudhuri, Amitabha

APPLICANT: Edinger, Shlomit

APPLICANT: Gerlach, Valerie

APPLICANT: Giot, Loic

APPLICANT: Gorman, Linda

APPLICANT: Guo, Xiaojia

APPLICANT: Kekuda, Ramesh

APPLICANT: Mezes, Peter

APPLICANT: Millet, Isabelle

APPLICANT: Ooi, Chean Eng

APPLICANT: Patturajan, Meera

APPLICANT: Rieger, Daniel

APPLICANT: Spytek, Kimberly

APPLICANT: Taupier Jr., Raymond J.

APPLICANT: Zerhusen, Bryan

APPLICANT: Zhong, Haihong

APPLICANT: Zhong, Mei

TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS C

FILE REFERENCE: 21402-462D

CURRENT APPLICATION NUMBER: US/10/262,445

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: 60/327,454

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/328,029

PRIOR FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/328,056

PRIOR FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/328,849

PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/329,414

PRIOR FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 60/330,142

PRIOR FILING DATE: 2001-10-17

PRIOR APPLICATION NUMBER: 60/341,058

PRIOR FILING DATE: 2001-10-22

PRIOR APPLICATION NUMBER: 60/343,629

PRIOR FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: 60/349,575

2n-1 = 128
2n = 129

! PRIOR FILING DATE: 2001-10-29
! Remaining Prior Application data removed - See File Wrapper or PALM.

! NUMBER OF SEQ ID NOS: 133
! SOFTWARE: CuraseqList version 0.1
! SEQ ID NO 128
! LENGTH: 227
! TYPE: PRT
! ORGANISM: Homo sapiens
US-10-262-445-128

Query Match 100.0%; Score 1192; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.6e-100;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Qy 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Db 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLAVTESKGHSE 180
Db 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLAVTESKGHSE 180
Qy 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227

RESULT 2

US-10-780-043-6
! Sequence 6, Application US/10780043
! Publication No. US20040137506A1
! GENERAL INFORMATION:
! APPLICANT: Bates, Elizabeth
! APPLICANT: Fournier, Nathalie
! APPLICANT: Chalus, Lionel
! APPLICANT: Garrone, Pierre
! TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
! FILE REFERENCE: SF0977X
! CURRENT FILING DATE: 2004-02-17
! PRIOR FILING DATE: 2004-02-17
! PRIOR APPLICATION NUMBER: US/09/869,388
! PRIOR FILING DATE: 2002-02-21
! NUMBER OF SEQ ID NOS: 14
! SOFTWARE: IBM PC compatible
! SEQ ID NO 6
! LENGTH: 227
! TYPE: PRT
! ORGANISM: homo sapiens
US-10-780-043-6

Query Match 100.0%; Score 1192; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.6e-100;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Qy 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Db 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLAVTESKGHSE 180
Db 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLAVTESKGHSE 180
Qy 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227

RESULT 3

US-10-820-474A-7
! Sequence 7, Application US/10820474A
! Publication No. US20050155089A1
! GENERAL INFORMATION:
! APPLICANT: LAL, PREETI
! APPLICANT: TANG, Y. TOM
! APPLICANT: GORGONE, GINA A.
! APPLICANT: CORLEY, NEIL C.
! APPLICANT: GUEGLER, KARL J.
! APPLICANT: BAUGHN, MARIAH R.
! APPLICANT: AKERBLOM, INGRID E.
! APPLICANT: AU-YOUNG, JANICE
! APPLICANT: YUE, HENRY
! APPLICANT: PATTERSON, CHANDRA
! APPLICANT: REDDY, ROOPA
! APPLICANT: HILLMAN, JENNIFER L.
! APPLICANT: BANDMAN, OLGA

! TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING MOLECULES
! FILE REFERENCE: 039386-1568
! CURRENT APPLICATION NUMBER: US/10/820,474A
! CURRENT FILING DATE: 2004-04-07
! PRIOR APPLICATION NUMBER: 09/720,533
! PRIOR FILING DATE: 2001-03-20
! PRIOR APPLICATION NUMBER: PCT/US99/14484
! PRIOR FILING DATE: 1999-06-25
! PRIOR APPLICATION NUMBER: 60/090,762
! PRIOR FILING DATE: 1998-06-26
! PRIOR APPLICATION NUMBER: 60/094,983
! PRIOR FILING DATE: 1998-07-31
! PRIOR APPLICATION NUMBER: 60/102,686
! PRIOR FILING DATE: 1998-10-01
! NUMBER OF SEQ ID NOS: 269
! SOFTWARE: PatentIn version 3.3
! SEQ ID NO 7
! LENGTH: 227
! TYPE: PRT
! ORGANISM: Homo sapiens
! NAME/KEY: misc feature
! OTHER INFORMATION: Incyte Clone No: 962390
US-10-820-474A-7

Query Match 100.0%; Score 1192; DB 5; Length 227;
Best Local Similarity 100.0%; Pred. No. 6.6e-100;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
Qy 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Db 61 LAIVPNVRISWRGRGHFGQSFYSTRPPIHDKYVNRFLNWTQESGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLAVTESKGHSE 180
Db 121 SVYFCRVELDTRRSGRQQLQSIKGTCLTITQAVTTTTTWRPSSTTTTLAVTESKGHSE 180
Qy 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVAVLKTIVILGLLCLLLLMWRRRKGSRAPSSDF 227

RESULT 4

US-05-935-390A-21
! Sequence 21, Application US/09935390A
! Patent No. US20020076761A1
! GENERAL INFORMATION:
! APPLICANT: Escobedo, Jaime
! Quianjin, Hu

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1192	100.0	227	3	AA807445	Aab07445 A human m
2	1192	100.0	227	6	AAU89824	Abu89824 TNP-recep
3	1192	100.0	291	2	AAW63682	Aaw63682 Human sec
4	1192	100.0	326	4	ABBL12010	Abbl12010 Human sig
5	1179	98.9	227	3	AAV87230	Aav87230 Human sig
6	1163.5	97.6	226	2	AAV08015	Aay08015 Human LSP
7	1163.5	97.6	226	3	AAW07447	Aab07447 A human m
8	1157.5	97.1	226	2	AAW80407	Aaw80407 A secrete
9	1157.5	97.1	226	5	ABP61825	Abp61825 Human pol
10	1069	89.7	238	5	ABG95345	Abg95345 Human nov
11	1069	89.7	238	6	ABO34539	AbO34539 Region of
12	1069	89.7	238	7	AD123200	Adi23200 Novel hum
13	1069	89.7	238	8	ADH74202	Adh74202 Human sec
14	958	80.4	303	2	AAW62772	Aaw62772 Human imm
15	958	80.4	303	3	AAW07443	Aab07443 A human m
16	958	80.4	303	8	ADP25129	Adp25129 PRO polyg
17	752	63.1	1012	4	ABG00509	Abg00509 Novel hum
18	752	63.1	1012	4	ABG16869	Abg16869 Novel hum
19	752	63.1	1012	4	ABG02851	Abg02851 Novel hum
20	752	63.1	1012	4	ABG21403	Abg21403 Novel hum
21	744	62.4	228	8	ADK98565	Adk98565 Human imm
22	744	62.4	230	3	AAW07444	Aab07444 A human m
23	744	62.4	230	7	ADB95578	AdB95578 Human NOV
24	742.5	62.3	175	3	AAW07446	Aab07446 A human m

CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocysteine-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocyte hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 1192; DB 3; Length 227;
 Best Local Similarity 100.0%; Pred. No. 5e-97;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGRPLLLPALLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 DB 1 MGRPLLLPALLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60
 QY 61 LAIVPNVRISWRGRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEQSGSGLRISNLRKEDQ 120
 DB 61 LAIVPNVRISWRGRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEQSGSGLRISNLRKEDQ 120
 QY 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
 DB 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180
 QY 181 SWHLSLDTAIRVALAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 227
 DB 181 SWHLSLDTAIRVALAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 227

RESULT 2
 ABU89824

ID ABU89824 standard; protein; 227 AA.

AC ABU89824;

DT 10-JUL-2003 (first entry)

DE TNF-receptor associated factor 5 (TRAF5) interacting protein #4.

KW Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer;

KW TNF-receptor associated factor 5 interacting protein;

KW tumour necrosis factor associated factor 5 interacting protein;

KW TRAF5 interacting protein.

OS Homo sapiens.

XX WO20003031571-A2.

PD 17-APR-2003.

PF 02-OCT-2002; 2002WO-US031357.

XX 05-OCT-2001; 2001US-0327454P.

PR 09-OCT-2001; 2001US-0327917P.

PR 09-OCT-2001; 2001US-0328029P.

PR 09-OCT-2001; 2001US-0328056P.

PR 12-OCT-2001; 2001US-0328849P.

PR 15-OCT-2001; 2001US-0329414P.

PR 17-OCT-2001; 2001US-0330142P.

PR 22-OCT-2001; 2001US-0341058P.

PR 24-OCT-2001; 2001US-0343629P.

PR 29-OCT-2001; 2001US-0349575P.

PR 01-NOV-2001; 2001US-0346357P.

PR 25-JUN-2002; 2002US-0391342P.

PR 01-OCT-2002; 2002US-00262445.

XX (CURA-) CURAGEN CORP.

XX

PI Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;
 PI Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;
 PI Mezes PS, Millet I, Ooi CE, Patturajan M, Rieger DK, Spytek KA;
 PI Taupier RJ, Zehusen BD, Zhong H, Zhong M;
 XX WPI; 2003-381704/36.
 DR N-PSDB; ACA90240.
 XX New DAPK3 polypeptide, useful for preparing a composition for treating or
 PT preventing e.g., cancer.
 XX Example 20F; Page 242; 253pp; English.

XX The invention describes an isolated polypeptide comprising any of 33 90-
 CC 1273 amino acid sequences (I) given in the specification or its mature
 CC form, a sequence that is at least 95 % identical to (I), or a sequence
 CC comprising one or more conservative substitutions in the amino acid
 CC sequence of (I). The polypeptide is useful for preparing a composition
 CC for treating or preventing e.g. cancer. This is the amino acid sequence
 CC of a tumour necrosis factor (TNF)-receptor associated factor 5 (TRAF5)
 CC interacting protein associated with the identification of novel human
 CC proteins and their functions

XX SQ Sequence 227 AA;

Query Match 100.0%; Score 1192; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 5e-97;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPALLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60

DB 1 MGRPLLLPALLLPAPLQPGSGTSGPSYLYGVTPKHLASMGSGVEIPFSFYYPWE 60

QY 61 LAIVPNVRISWRGRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEQSGSGLRISNLRKEDQ 120

DB 61 LAIVPNVRISWRGRGHFGQSFYSTRPPSIHKDYVNRFLFNWTEQSGSGLRISNLRKEDQ 120

QY 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180

DB 121 SVYFCRVELDTRRSGRQLOSIKGTCLTITQAVTTTTTWRPSSTTTLAGLRVTSKGHSE 180

QY 181 SWHLSLDTAIRVALAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 227

DB 181 SWHLSLDTAIRVALAVLTKTVILGLLCLLLMWRRRKGRAPSSDF 227

RESULT 3
 AAW63682

ID AAW63682 standard; protein; 291 AA.

AC AAW63682;

XX 24-SEP-1998 (first entry)

DT Human secreted protein 2.

DE Secreted protein; human; cell proliferation; cytokine activity; inhibin;
 KW tissue growth; cellular differentiation; regeneration; activin;
 KW chemotactic; haemostatic; thrombolytic; tumour inhibition;
 KW anti-inflammatory activity; biomarker.

OS Homo sapiens.

XX WO9825959-A2.

PN 18-JUN-1998.

PD 11-DEC-1997; 97WO-US022787.

PR 11-DEC-1996; 96US-0032757P.

PR (CHIR) CHIRON CORP.

XX

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:08 ; Search time 15.8372 Seconds
(without alignments)
1379.107 Million cell updates/sec

Title: US-10-780-043-6

Perfect score: 1192

Sequence: 1 MGRPILLPLLLQLPPAFLO.....CLLLWRRKGRAPSSDF 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120.5	10.1	823	2 S48394	probable membrane
2	105.5	8.9	403	2 I52590	m33-B isoform - mo
3	104	8.7	1694	2 S50065	sialoadhesin - mou
4	103	8.6	240	2 JL0143	antigen BCM1 precu
5	101.5	8.5	392	1 RWHPD	poliovirus recepto
6	101.5	8.5	417	1 RWHPA	poliovirus recepto
7	100.5	8.4	478	2 I53960	PRR2 alpha - human
8	100.5	8.4	538	2 I68093	PRR2 delta - human
9	99	8.3	143	2 S36300	T-cell receptor de
10	99	8.3	210	2 E46482	T-cell surface gly
11	99	8.3	221	2 C46482	T-cell surface gly
12	99	8.3	246	2 D46482	T-cell surface gly
13	99	8.3	246	2 T01073	T cell surface gly
14	98.5	8.3	235	2 S14675	IG lambda chain -
15	98.5	8.3	772	2 T13078	KIAA0992 protein -
16	98	8.2	192	2 I33464	CD8 antigen - huma
17	98	8.2	210	2 S25657	T-cell surface gly
18	97	8.1	142	2 A28344	VpreB protein prec
19	96.5	8.1	1231	2 T18390	latrophilin-3, spl
20	96.5	8.1	1240	2 T18393	latrophilin-3, spl
21	96.5	8.1	1274	2 T18391	latrophilin-3, spl
22	96.5	8.1	1283	2 T18394	latrophilin-3, spl
23	96.5	8.1	1299	2 T18398	latrophilin-3, spl
24	96.5	8.1	1308	2 T18408	latrophilin-3, spl
25	96.5	8.1	1342	2 T18405	latrophilin-3, spl
26	96.5	8.1	1351	2 T18409	latrophilin-3, spl
27	96.5	8.1	1503	2 T18389	latrophilin-3, spl
28	96.5	8.1	1512	2 T18392	latrophilin-3, spl
29	96.5	8.1	1571	2 T18395	latrophilin-3, spl

30	96.5	8.1	1580	2 T18407	latrophilin-3, spl
31	96	8.1	392	2 B44194	poliovirus recepto
32	96	8.1	417	2 A44194	poliovirus recepto
33	95.5	8.0	145	2 S36299	T-cell receptor de
34	95	8.0	152	2 B26471	IG heavy chain pre
35	94	7.9	142	2 B28344	VpreB protein prec
36	93	7.8	122	2 H30535	IG heavy chain v r
37	92.5	7.8	119	2 D27889	IG heavy chain v r
38	92.5	7.8	132	2 P01114	IG lambda chain pr
39	92.5	7.8	142	2 S36310	T-cell receptor de
40	92	7.7	98	2 H47624	IG heavy chain v-I
41	91.5	7.7	213	2 A30585	T-cell surface gly
42	90.5	7.6	117	2 P02552	IG heavy chain v r
43	90.5	7.6	213	2 A34953	T-cell surface gly
44	90.5	7.6	710	2 A39486	ABC transporter, b
45	90.5	7.6	735	2 S76425	hypothetical prote

ALIGNMENTS

RESULT 1

S48394

probable membrane protein Y1L140w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004

C:Accession: S48394; S50276

R:Churcher, C.

submitted to the EMBL Data Library, September 1994

A:Reference number: S48310

A:Accession: S48394

A:Molecule type: DNA

A:Residues: 1-823 <CHU>

A:Cross-references: UNIPROT:P38928; UNIPARC:UPI000012669C; GB:Z47047; EMBL:Z38059; NID:9

R:Torpey, L.E.; Gibbs, P.E.M.; Nelson, J.; Lawrence, C.W.

Yeast 10, 1503-1509, 1994

A:Title: Cloning and sequence of REV7, a gene whose function is required for DNA damage-

A:Reference number: S50275; MUID:95176709; PMID:7871890

A:Accession: S50276

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 80-823 <TOR>

A:Cross-references: UNIPARC:UPI00001689D0; EMBL:U07228; NID:9460247; PIDN:AAA67919.1; P1

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994

C:Genetics:

A:Gene: SGD:SR04

A:Cross-references: SGD:S0001402; MIPS:Y1L140w

A:Map position: 9L

C:Superfamily: Saccharomyces cerevisiae probable membrane protein Y1L140w

C:Keywords: transmembrane protein

F:6-22/Domain: transmembrane #status predicted <TM1>

F:511-527/Domain: transmembrane #status predicted <TM2>

Query Match 10.1%; Score 120.5; DB 2; Length 823;
Best Local Similarity 23.0%; Pred. No. 0.022; Mismatches 85; Indels 73; Gaps 15;
Matches 60; Conservative 43;

QY 12 LIQPPAFIQPGST--GSGPSYLYGV-TQPKHLSASM---GGSVEIPFSFYFWE-----60

Db 293 LLDAPDWALDNATISGVSFDELLGKNPNANFSVIYDTYGDV-----IYFNFVWSTT 347

QY 61 ----LAIYVNVRIISWRGHFGHQSFSYTRPPIHKKDYVNR-----LFLN-----WTEGQE 106

Db 348 DLFAISLSLFINAT--RGEWFSYFL---PSQPTDYVNTVNSLFTNSSQDHDWVKFOS 401

QY 107 S-----GFLRIS-----NLKEDOSVYFCRVELDTR-----BSGRQQ 138

Db 402 SNLTLAGVPPKPNFKDLGLKANQSQSQEQLFYNTIGMDSKLTSHNSANATSTRSSSHS 461

QY 139 LQSIGTKLTITQAVTTTTTWRPSTTTIAGLRVTESKGHSWMHLSLDTAIRVALAVAV 198

Db 462 TSTSTSTSTYTTAKISSISA-AATSSAAPALPAANKTSSHVK-----AVAIACGVAI 513

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 97.9561 Seconds
(without alignments)
1634.967 Million cell updates/sec

Title: US-10-780-043-6

Perfect score: 1192

Sequence: 1 MGRPPLLPLLLQLPPAFLO.....CLLLWRRKGRAPSSDP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1192	100.0	227	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
2	958	80.4	303	Q9UKJ1_HUMAN	Q9ukj1 homo sapien
3	744	62.4	226	Q8NH11_HUMAN	Q8nh11 homo sapien
4	410	34.4	299	Q8BYA6_MOUSE	Q8bya6 mus musculus
5	123.5	10.4	633	Q5W434_BRARE	Q5w434 brachydanio
6	123.5	10.4	651	Q5W433_BRARE	Q5w433 brachydanio
7	120.5	10.1	823	AXL2_YEAST	P38328 saccharomyc
8	118	9.9	149	Q69YF9_HUMAN	Q69yf9 homo sapien
9	118	9.9	271	Q9HBS0_HUMAN	Q9hbso homo sapien
10	115.5	9.7	831	Q755V1_ASHGO	Q755v1 ashbya goss
11	111	9.3	275	Q41JC5_GIBZE	Q41jc5 gibberella
12	107.5	9.0	442	Q9BY67_HUMAN	Q9by67 homo sapien
13	106.5	8.9	295	Q92ZL8_MOUSE	Q92zl8 mus musculus
14	106.5	8.9	445	Q84L11_MOUSE	Q84l11 mus musculus
15	105.5	8.9	403	CD33_MOUSE	Q63994 mus musculus
16	104	8.7	1694	SN_MOUSE	Q62230 mus musculus
17	103.5	8.7	233	Q8TBC9_HUMAN	Q8tbc9 homo sapien
18	103.5	8.7	369	Q7YUQ4_9TRYP	Q7yuq4 trypanosoma
19	103.5	8.7	445	Q8K3T6_MOUSE	Q8k3t6 mus musculus
20	103	8.6	240	CD48_MOUSE	P18181 mus musculus
21	103	8.6	240	Q545K2_MOUSE	Q545k2 mus musculus
22	103	8.6	240	Q6P905_MOUSE	Q6p905 mus musculus
23	103	8.6	397	GATAS5_HUMAN	Q9bwx5 homo sapien
24	103	8.6	417	Q86VU4_HUMAN	Q86vu4 homo sapien
25	102.5	8.6	151	Q8C2T1_MOUSE	Q8c2t1 mus musculus
26	102.5	8.6	283	Q5DMN5_EPTBU	Q5dmn5 eptatretus
27	102.5	8.6	283	Q5DMN6_EPTBU	Q5dmn6 eptatretus
28	102.5	8.6	369	Q7YUQ1_9TRYP	Q7yuq1 trypanosoma
29	101.5	8.5	359	Q5R1X6_RAT	Q5r1x6 rattus norv
30	101.5	8.5	369	Q7YUQ2_9TRYP	Q7yuq2 trypanosoma
31	101.5	8.5	370	Q4KCC5_PSEB5	Q4kcc5 pseudomonas

32	101.5	8.5	417	1	PVR_HUMAN	P15151 homo sapien
33	101.5	8.5	595	2	Q5W431_FUGRU	Q5w431 fugu rubrip
34	101.5	8.5	630	2	Q5W436_FUGRU	Q5w436 fugu rubrip
35	101.5	8.5	648	2	Q5W435_FUGRU	Q5w435 fugu rubrip
36	100.5	8.4	236	2	Q6PIQ7_HUMAN	Q6piq7 homo sapien
37	100.5	8.4	347	2	Q60H11_EPTBU	Q60h11 eptatretus
38	100.5	8.4	369	2	Q7YUQ3_9TRYP	Q7yuq3 trypanosoma
39	100.5	8.4	479	2	Q6IB16_HUMAN	Q6ib16 homo sapien
40	100.5	8.4	538	1	PVR2_HUMAN	Q92692 homo sapien
41	100	8.4	341	2	Q819K3_BRAFL	Q819k3 brachiosteo
42	100	8.4	401	2	Q08835_CERAE	Q08835 cercopithe
43	99.5	8.3	289	2	Q6GX36_MOUSE	Q6gx36 mus musculu
44	99.5	8.3	356	2	Q8AXL7_ONCMY	Q8axl7 oncorhynchu
45	99.5	8.3	359	1	HPLN3_MOUSE	Q80wm5 mus musculu

ALIGNMENTS

RESULT 1

Q9UKJ0_HUMAN
ID Q9UKJ0_HUMAN PRELIMINARY; PRT; 227 AA.
AC Q9UKJ0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE Activating receptor PILRBeta (Hypothetical protein DKFZp340O079).
GN Name=DKFZp340O079;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banyville D., L'Abbe D., Moosmayer P., Schupp I., Wellenreuther R., Poustka A., Albert R., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Mewes H.W., Weil B.,
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- INTERACTION: O95870:BAT5; NbExp=1; IntAct=EBI-347958, EBI-348517;
EMBL; AP161081; AAD52965.1; -; mRNA.
EMBL; AL834336; CAH10711.1; -; mRNA.
IntAct; Q9UKJ0; -.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007171; F:transmembrane receptor protein tyrosine kin. . .; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein; Immunoglobulin domain; Receptor.
SQ SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7BF09 CRC64;

Query Match 100.0%; Score 1192; DB 2; Length 227;

Best Local Similarity 100.0%; Pred. No. 4e-101;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPPLLPLLLQLPPAFLOPCGSGSGSYLYGVTPKHLASMGSGSVEIPFSFYFWE 60

DB 1 MGRPPLLPLLLQLPPAFLOPCGSGSGSYLYGVTPKHLASMGSGSVEIPFSFYFWE 60

QY 61 LAIVFNVRISWRGHFGQSFSYTPPSIHKKDYVRLFNWTEGSGSLRISNLKEDQ 120

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Db 61 LAIPVNRVIRSWRGHFGHQSFSYSTRPSPSIHKDYVNRFLFNWTEGQSGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSRGROQLQSGTKLTIQAVTTTTWRPSSTTTLAGLVTSKGHSE 180
Db 121 SVYFCRVELDTRRSRGROQLQSGTKLTIQAVTTTTWRPSSTTTLAGLVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVAVLTKTVILGCLLLLMWRRRKGSRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVAVLTKTVILGCLLLLMWRRRKGSRAPSSDF 227

RESULT 2
Q9UKJ1 HUMAN
ID Q9UKJ1 HUMAN PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inhibitory receptor PILRALpha.
GN Name=PILRA;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
paired with the truncated counterpart PILRBeta.";
EL J. Biol. Chem. 275:4467-4474(2000)
DR EMBL, AF161080; AAD2964.1; -; mRNA.
DR Ensembl; ENSG0000085514; Homo sapiens.
DR HGNC; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; P:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; ISS.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 303 AA; 33878 MW; 0410ADF7E80928B CRC64;

Query Match 80.4%; Score 958; DB 2; Length 303;
Best Local Similarity 80.8%; Pred. No. 1.8e-79;
Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;

Qy 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Qy 61 LAIPVNRVIRSWRGHFGHQSFSYSTRPSPSIHKDYVNRFLFNWTEGQSGFLRISNLRKEDQ 120
Db 61 LATAPDVIRISWRGHHFGHQSFSYSTRPSPSIHKDYVNRFLFNWTEGQSGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSRGROQLQSGTKLTIQAVTTTWRPSSTTTLAGLV 172
Db 121 SVYFCRVELDTRRSRGROQLQSGTKLTIQAVTTTWRPSSTTTLAGLV 180

Qy 173 TESKGHSSWHLSDTAIRVALAVAVLTKTVILGCLLLLMWRRRKGSR 221
Db 181 TGKRRSDSWHLSLETAGVAVAVTVILGILGLICLLR--WRRRKGQ 227

RESULT 3
Q8NH11 HUMAN
ID Q8NH11 HUMAN PRELIMINARY; PRT; 226 AA.
AC Q8NH11
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
```

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OS PILRA protein.
DB Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Boeak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC TISSUE=Lung;
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017812; AAH17812.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;

Query Match 62.4%; Score 744; DB 2; Length 226;
Best Local Similarity 86.4%; Pred. No. 5.6e-60;
Matches 140; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Db 1 MGRPLLLPLLLLOPPAPLQPGSGTSGPSYLYGVTPQKHLASMGGSVEIPFSFYYPWE 60
Qy 61 LAIPVNRVIRSWRGHFGHQSFSYSTRPSPSIHKDYVNRFLFNWTEGQSGFLRISNLRKEDQ 120
Db 61 LATAPDVIRISWRGHHFGHQSFSYSTRPSPSIHKDYVNRFLFNWTEGQSGFLRISNLRKEDQ 120
Qy 121 SVYFCRVELDTRRSRGROQLQSGTKLTIQAVTTTWRPSS 162
Db 121 SVYFCRVELDTRRSRGROQLQSGTKLTIQAVTTTWRPSS 162

RESULT 4
Q8BYA6 MOUSE
ID Q8BYA6 MOUSE PRELIMINARY; PRT; 299 AA.
AC Q8BYA6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630007P20 product:weakly similar to INHIBITORY
DE RECEPTOR PILRALPHA.
GN Name=Pilra; Synonyms=AV021745;
OS Mus musculus (Mouse).
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 23.6581 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-6

Perfect score: 1192

Sequence: 1 MGRPILLPLLLLOPPAFLO.....CLLLWRRRKGSRAPSSDF 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgn2_6/ptodata/1/1aa/6-COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/H-COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/PCUS-COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/R8-COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1192	100.0	227	2	US-09-869-388-6
2	1163.5	97.6	226	2	US-09-869-388-10
3	1069	89.7	238	2	US-09-149-478-485
4	958	80.4	303	2	US-08-985-950-2
5	958	80.4	303	2	US-09-546-049-2
6	958	80.4	303	2	US-09-869-388-2
7	744	62.4	230	2	US-09-869-388-4
8	742.5	62.3	175	2	US-09-869-388-8
9	532	44.6	101	2	US-09-149-478-754
10	223	18.7	99	2	US-08-985-950-4
11	223	18.7	99	2	US-09-546-049-4
12	114	9.6	143	1	US-08-345-321-8
13	112	9.4	352	2	US-09-203-958A-2
14	110.5	9.3	310	2	US-09-079-029-11
15	107.5	9.0	440	2	US-09-866-028-61
16	107.5	9.0	440	2	US-09-944-457-61
17	107.5	9.0	440	2	US-09-945-584-61
18	107.5	9.0	440	2	US-09-944-944-61
19	107.5	9.0	440	2	US-09-945-587-61
20	107.5	9.0	442	2	US-09-778-510-20
21	107.5	9.0	442	2	US-09-930-803-1
22	107	9.0	476	2	US-09-291-299A-3
23	106.5	8.9	423	2	US-09-778-510-22
24	106	8.9	354	2	US-09-393-627B-28
25	105.5	8.9	244	2	US-08-918-148-79
26	105.5	8.9	244	2	US-09-138-091A-77
27	101.5	8.5	284	2	US-08-564-164A-2

28 101.5 8.5 417 2 US-09-949-016-6729 Sequence 6729, Ap
29 101.5 8.5 456 2 US-09-949-016-7564 Sequence 7564, Ap
30 101 8.5 280 2 US-09-260-527-1 Sequence 1, Appl
31 100.5 8.4 479 2 US-09-723-368-2 Sequence 2, Appl
32 100.5 8.4 479 2 US-09-949-016-6278 Sequence 6278, Ap
33 100.5 8.4 522 2 US-09-949-016-7563 Sequence 7563, Ap
34 99.5 8.3 225 2 US-09-456-090A-66 Sequence 66, Appl
35 99.5 8.3 225 2 US-09-453-234-66 Sequence 66, Appl
36 99.5 8.3 312 2 US-09-079-029-10 Sequence 10, Appl
37 99 8.3 265 1 US-08-403-853-16 Sequence 16, Appl
38 99 8.3 355 2 US-08-875-811-57 Sequence 57, Appl
39 98.5 8.3 421 2 US-08-759-628-5 Sequence 5, Appl
40 98.5 8.3 622 1 US-08-356-785-16 Sequence 16, Appl
41 98 8.2 159 1 US-08-653-402B-2 Sequence 2, Appl
42 98 8.2 225 2 US-09-456-090A-70 Sequence 70, Appl
43 98 8.2 225 2 US-09-453-234-70 Sequence 70, Appl
44 98 8.2 360 2 US-09-907-794A-213 Sequence 213, App
45 98 8.2 360 2 US-09-905-125A-213 Sequence 213, App

ALIGNMENTS

RESULT 1
US-09-869-388-6
; Sequence 6, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 6
; LENGTH: 227
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-6

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Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MGRPILLPLLLLOPPAFLOPGSGTSGPSYLYGVTPKHLASMGSGVEIPSFYYPWE 60
Qy 61 LAIVPNVRISWRRGHFGQSFYSTRPPSIHKDYVNRFLPNWTGQSGFLRISNLRKEDQ 120
Db 61 LAIVPNVRISWRRGHFGQSFYSTRPPSIHKDYVNRFLPNWTGQSGFLRISNLRKEDQ 120
Qy 121 SYVFCRVELDTRSRGRQQLQSIKTKLTITQAVTTTTTWRPSTTTTITAGLRVTSKGHSE 180
Db 121 SYVFCRVELDTRSRGRQQLQSIKTKLTITQAVTTTTTWRPSTTTTITAGLRVTSKGHSE 180
Qy 181 SWHLSLDTAIRVALAVAVKTVILGLCLLLWRRRKGSRAPSSDF 227
Db 181 SWHLSLDTAIRVALAVAVKTVILGLCLLLWRRRKGSRAPSSDF 227

RESULT 2
US-09-869-388-10
; Sequence 10, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel

APPLICANT: Garrone, Pierre
FILE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
FILE REFERENCE: SF0977X
CURRENT APPLICATION NUMBER: US/09/869,388
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: IBM PC compatible
SEQ ID NO 10
LENGTH: 226
TYPE: PRT
ORGANISM: homo sapiens
US-09-869-388-10

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Best Local Similarity 98.2%; Pred. No. 1.3e-111;
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Qy 121 SVYFCRVELDRRSRQQLQSIKTKLTITQAVTTTTTWRPSSITTIAGLRVTSKGHSE 180
Db 121 SVYFCRVELDRRSRQQLQSIKTKLTITQAVTTTTTWRPSSITTIAGLRVTSKGHSE 180

Qy 181 SWHLSLDTAIRVALAVAVLTKTVILGLLCLLLWRRRKGSRAPSSDP 227
Db 181 SWHLSLDTAIRVALAVAVLTKTVILGLLCLLLWRRRKGSRAPSSDF 226

RESULT 3
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Sequence 485, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 166 Human Secreted proteins
FILE REFERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22

GenCore version 5.1.6
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Run on: December 23, 2005, 20:18:33 ; Search time 95.6848 Seconds
(without alignments)
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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*
9: Geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	1173.5	96.0	303	8	ADP25129 PRO polyp
6	1057	86.4	206	7	AD95580 Human NOV
7	974	79.6	228	8	ADK98565 Human imm
8	830	67.9	1012	4	ABG00509 Novel hum
9	830	67.9	1012	4	ABG16869 Novel hum
10	830	67.9	1012	4	ABG02851 Novel hum
11	830	67.9	1012	4	ABG21403 Novel hum
12	816	66.7	175	3	AAB07446 A human m
13	765	62.6	226	2	AAW80407 A secrete
14	765	62.6	226	5	ABP61825 Human pol
15	759	62.1	226	2	AAV08015 Human LSP
16	759	62.1	226	3	AAB07447 A human m
17	745	60.9	238	5	ABG95345 Human nov
18	745	60.9	238	6	ABO34539 Region of
19	745	60.9	238	7	AD123200 Novel hum
20	745	60.9	238	8	ADH74202 Human sec
21	744	60.8	227	3	AAB07445 A human m
22	744	60.8	227	6	ABU98824 TNF-recep
23	744	60.8	291	2	Aaw63682 Human sec
24	744	60.8	326	4	ABB12010 Human sec

RESULT 1
AAB07444
ID AAB07444 standard; protein; 230 AA.
XX AAB07444;
AC AAB07444;
XX
DT 20-OCT-2000 (first entry)
XX
DB A human monocyte-derived protein PDF03Deltatm.
XX
KW Human; monocyte-derived protein; PDF03; PDF03Deltatm; PDF03-S1;
PDF03-M14; PDF03-S2; haematopoietic cell; monocyte hyperplasia;
tissue rejection; inflammation; infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT Protein /note= "signal peptide"
18..230
FT Protein /note= "mature protein"
XX
PN WO2000040721-A1.
XX
PD 13-JUL-2000.
XX
PF 29-DEC-1999; 99WO-US030004.
XX
PR 31-DEC-1998; 98US-00223919.
31-DEC-1998; 98US-00224604.
XX
PA (SCHE) SCHERING CORP.
XX
PI Bates E, Fournier N, Chaulus L, Garrone P;
XX
DR WPI; 2000-465984/40.
DR N-PSDB; AAA58815.
XX
PT Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
PT diseases associated with changes in monocyte numbers, e.g. bacterial or
XX viral infections.
XX
PS Claim 1; Page 34-35; 45pp; English.
XX
CC The present sequence represents a human monocyte-derived protein. The
specification describes monocyte-derived proteins PDF03, PDF03Deltatm,
PDF03-S1, PDF03-M14, and PDF03-S2. The proteins are involved in the

ALIGNMENTS

25	731	59.8	227	3	AAV87230	Aay97230 Human sig
26	517	42.3	101	2	AAW75053	Aaw75053 Fragment
27	517	42.3	101	5	ABG95614	Abg95614 Human nov
28	517	42.3	101	6	ABO34808	AbO34808 Fragment
29	517	42.3	101	7	ADI23469	Adi23469 Novel hum
30	517	42.3	101	8	ADH74471	Adh74471 Human sec
31	354	28.9	224	5	ABB72387	Abb72387 Murine pr
32	348.5	28.5	212	7	ADE59537	Ades9537 Rat prote
33	222	18.2	99	2	AAW62773	Aaw62773 Partial m
34	120	9.8	577	4	AAU19872	Aabi9872 Activatin
35	116.5	9.5	253	6	ABU97144	Abu97144 Recombina
36	115.5	9.4	247	6	ABU97118	Abu97118 Recombina
37	115.5	9.4	1700	5	ABO5044	Abb05044 Human NOV
38	115.5	9.4	1700	8	ADH71518	Adh71518 Human pro
39	115.5	9.4	1700	8	ADH71522	Adh71522 Human pro
40	115.5	9.4	1700	8	ADH71502	Adh71502 Human pro
41	115.5	9.4	1700	8	ADH71520	Adh71520 Human pro
42	115.5	9.4	1700	8	ADH71516	Adh71516 Human pro
43	114.5	9.4	252	6	ABU97128	Abu97128 Recombina
44	114.5	9.4	253	6	ABU97134	Abu97134 Recombina
45	114.5	9.4	253	8	ADS09256	Ads09256 Human C-M

CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocytic-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocytic hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX Sequence 230 AA;

Query Match 100.0%; Score 1223; DB 3; Length 230;
 Best Local Similarity 100.0%; Pred. No. 5.1e-97;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFFSYFWE 60
 Db 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFFSYFWE 60
 Qy 61 LATAPDVRIWRRGHFGQSPYSTRPPIHDKYVNRFLNWTGKSGFLRISNLQKDD 120
 Db 61 LATAPDVRIWRRGHFGQSPYSTRPPIHDKYVNRFLNWTGKSGFLRISNLQKDD 120
 Qy 121 SVYFCRVELDRSSGRQWQSIETGKLSITQGGTQKATTPAREPFPQNTPEYINRNEG 180
 Db 121 SVYFCRVELDRSSGRQWQSIETGKLSITQGGTQKATTPAREPFPQNTPEYINRNEG 180
 Qy 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSVLKA 230
 Db 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSVLKA 230

RESULT 2

ID ADE95578
 AD ADE95578 standard; protein; 230 AA.

AC ADE95578;

DT 12-FEB-2004 (first entry)

DE Human NOVX18a protein.

XX NOVX protein; biochemical stimulation; physiological stimulation;
 KW cardiant; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
 KW antiinflammatory; anti-HIV; antidiabetic; nephrotropic; dermatological;
 KW immunosuppressive; anti-HIV; antiparkinsonian; antiaesthetic; neuroleptic;
 KW antipsychotic; antiparkinsonian; antiaesthetic; neuroleptic;
 KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
 KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; hypertension;
 KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
 KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
 KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
 KW depression; allergy; fertility disorder; NOVX18a.

OS Homo sapiens.

XX WO2003050245-A2.

XX 19-JUN-2003.

XX 03-DEC-2002; 2002WO-03038594.

XX 05-DEC-2001; 2001US-0336600P.

PR 07-DEC-2001; 2001US-0338285P.

PR 12-DEC-2001; 2001US-0341346P.

PR 17-DEC-2001; 2001US-0341477P.

PR 17-DEC-2001; 2001US-0341540P.

PR 20-DEC-2001; 2001US-0342592P.

PR 27-DEC-2001; 2001US-0344297P.

PR 31-DEC-2001; 2001US-0344903P.

PR 17-APR-2002; 2002US-0373288P.

PR 15-MAY-2002; 2002US-0380981P.
 PR 17-MAY-2002; 2002US-0381495P.
 PR 28-MAY-2002; 2002US-0383334P.
 PR 28-MAY-2002; 2002US-0383744P.
 PR 29-MAY-2002; 2002US-0383829P.
 PR 29-MAY-2002; 2002US-0384024P.
 PR 07-AUG-2002; 2002US-0401788P.
 PR 26-AUG-2002; 2002US-0406353P.
 PR 31-OCT-2002; 2002US-00401788.
 PR 02-DEC-2002; 2002US-00406353.
 XX

PA (CURA-) CURAGEN CORP.

XX Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;
 PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
 PI Jeffers WB, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;
 PI Patturajan M, Feyman JA, Rastelli L, Rieger DK, Shenoy SG;
 PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
 XX WPI; 2003-513974/48.
 DR N-PSDB; ADE95577.

XX New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.

PS Claim 2; SEQ ID NO 110; 211pp; English.

XX This invention relates to novel NOVX proteins, and the DNA sequence which
 CC encode them, having properties related to stimulation of biochemical or
 CC physiological responses in a cell, a tissue, an organ or an organism.
 CC Compounds which modulate the proteins of the invention may have cardiant,
 CC antiarteriosclerotic, hypotensive, cytostatic, anorectic, antineumatic,
 CC antiarthritic, antidiabetic, nephrotropic, dermatological,
 CC immunosuppressive, anti-HIV, antiparkinsonian, antiaesthetic, neuroleptic,
 CC antidepressant, antiallergic or gynaecological activities. The DNA
 CC sequences of the invention may be useful for gene therapy whilst the
 CC protein sequences may allow the development of a vaccine. The protein is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease. The invention may be useful in
 CC diagnosing, treating or preventing NOVX-associated disorders, for example
 CC cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
 CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
 CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
 CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
 CC fertility disorders. The nucleic acids may further be used as
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive
 CC medicine, and pharmacogenomics. The present sequence is the amino acid
 CC sequence of the human NOVX18a protein of the invention.

XX Sequence 230 AA;

Query Match 99.6%; Score 1218; DB 7; Length 230;
 Best Local Similarity 99.6%; Pred. No. 1.4e-96;
 Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFFSYFWE 60
 Db 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFFSYFWE 60
 Qy 61 LATAPDVRIWRRGHFGQSPYSTRPPIHDKYVNRFLNWTGKSGFLRISNLQKDD 120
 Db 61 LATAPDVRIWRRGHFGQSPYSTRPPIHDKYVNRFLNWTGKSGFLRISNLQKDD 120
 Qy 121 SVYFCRVELDRSSGRQWQSIETGKLSITQGGTQKATTPAREPFPQNTPEYINRNEG 180
 Db 121 SVYFCRVELDRSSGRQWQSIETGKLSITQGGTQKATTPAREPFPQNTPEYINRNEG 180
 Qy 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSVLKA 230
 Db 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRPLKSPQNETLYSVLKA 230

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:08 ; Search time 16.0465 Seconds
(without alignments)
1379.107 Million cell updates/sec

Title: US-10-780-043-4

Perfect score: 1223

Sequence: 1 MGRPLLLPLLLPLPPAPLQ.....PSHRPLKSPQNETLYSLVLA 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	8.9	1694	2 S50065	sialoadhesin - mou
2	104.5	8.5	572	2 B46529	Ig Y heavy chain (
3	101	8.3	118	2 E27889	Ig heavy chain V r
4	100.5	8.2	151	2 I46626	rearranged T-cell
5	99	8.1	235	2 S25758	Ig lambda chain -
6	98	8.0	882	2 I38912	receptor tyrosine
7	97.5	8.0	416	2 A54017	colon carcinoma-as
8	97.5	8.0	1209	2 T42718	probable neural ce
9	97	7.9	135	2 S33598	Ig gamma-2 chain -
10	97	7.9	142	2 A28344	VpreB protein prec
11	96.5	7.9	110	2 S57442	Ig lambda chain V-
12	96.5	7.9	7962	2 I38346	elastic titin - hu
13	96	7.8	226	2 A64777	membrane-bound inm
14	95.5	7.8	142	2 B28344	VpreB protein prec
15	95.5	7.8	152	2 B26471	Ig heavy chain pre
16	94.5	7.7	132	2 A54410	Ig light chain V r
17	94	7.7	890	1 A53743	protein-tyrosine k
18	93.5	7.6	131	2 S36301	T-cell receptor de
19	93.5	7.6	132	2 PL0114	Ig lambda chain pr
20	93.5	7.6	132	2 S04937	Ig lambda chain pr
21	93	7.6	119	2 D27889	Ig heavy chain V r
22	93	7.6	132	2 I71935	MHC class II I-A-a
23	93	7.6	140	2 I46638	rearranged T-cell
24	93	7.6	142	2 S36316	T-cell receptor de
25	93	7.6	240	2 JLO143	antigen BGM1 precu
26	93	7.6	403	2 I52590	m33-B isoform - mo
27	93	7.6	26926	1 I38344	titin, cardiac mus
28	92.5	7.6	111	1 L218UH	Ig lambda chain V-
29	92.5	7.6	136	2 S16848	Ig lambda chain V-

30	92	7.5	125	2 A31493	Ig light chain pre
31	91.5	7.5	137	2 S36311	T-cell receptor de
32	91.5	7.5	233	2 S25747	Ig lambda chain -
33	91	7.4	112	2 S31515	Ig lambda chain V
34	91	7.4	113	1 L1CHV	Ig lambda chain pr
35	91	7.4	145	2 S36299	T-cell receptor de
36	90.5	7.4	118	2 S04519	Ig lambda chain pr
37	90.5	7.4	235	2 S14675	Ig lambda chain -
38	90	7.4	110	2 S51149	antibody light cha
39	90	7.4	112	2 S44105	Ig lambda chain V-
40	90	7.4	135	2 S36298	T-cell receptor de
41	90	7.4	143	2 S36300	T-cell receptor de
42	90	7.4	149	2 S36317	T-cell receptor de
43	90	7.4	880	1 JCA166	protein-tyrosine k
44	90	7.4	1333	2 I78875	receptor tyrosine
45	90	7.4	2124	2 A28452	proteoglycan core

ALIGNMENTS

RESULT 1

S50065

sialoadhesin - mouse

C:Species: Mus musculus (house mouse)

C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S50065

R:Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; M1

EMBO J. 13, 4490-4503, 1994

A:Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells

A:Reference number: S50065; MUID:95009950; PMID:7925291

A:Accession: S50065

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1694 <CRO>

A:Cross-references: UNIPROT:Q62230; UNIPARC:UPI000028874; EMBL:Z36293; NID:G557253; PFI

Query Match

Best Local Similarity 8.9%; Score 109; DB 2; Length 1694;

Matches 38; Conservative 30; Mismatches 77; Indels 24; Gaps 6;

QY 33 VGVTPKHLASMGSGVEIPSPFYYPWELATAPDVRIISWRGHFHQS-----FYSTPR 86

Db 21 MGVSSPKNVQGLSGCLLIPCFISYPADVPVSNGITAIW-----YYDSKGRQVVIHSGDP 76

QY 87 PSIHKDYVNRLLFNWTEGQKSGFLRISNLQKQDSVYFCRVELDTRSSGRQWQSTEGTK 146

Db 77 KLVDKRFGRRAELMGMDHKVCNLLKDKLPEDSGTYNPRFEI---SDSNRLVDVKGTT 132

QY 147 LSITGQQRKTATTP--AREPQ---NTEEPY-----ENIRVEGQNTDP 185

Db 133 VTVTTDPSPTTITPEELREGMERNFNCSTPYLCLQEKQVSLQWRGQDP 181

RESULT 2

B46529

Ig Y heavy chain (7.8S) - duck

N:Alternate names: Ig gamma chain (7.8S)

C:Species: Anas platyrhynchos (domestic duck)

C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000

C:Accession: B46529; S20759

R:Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.

J. Immunol. 149, 2627-2633, 1992

A:Title: Structural relationship between the two IGY of the duck, Anas platyrhynchos: m

A:Reference number: A46529; MUID:93017865; PMID:1401901

A:Accession: B46529

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-572 <MAG>

A:Cross-references: UNIPARC:UPI0000116038; EMBL:X65219; NID:G62442; PIDN:CAA46322.1; PFI

A:Experimental source: spleen

A>Note: sequence extracted from NCBI backbone (NCBIP:116127)

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin
F/37-120/Domain: immunoglobulin homology <IMM>

Query Match 8.5%; Score 104.5; DB 2; Length 572;
Best Local Similarity 22.2%; Pred. No. 0.51;
Matches 49; Conservative 36; Mismatches 91; Indels 45; Gaps 10;

Qy 5 LLLPPLLPPAPLPQSGSGSPSYLYGVTPQKHLASMGSGSVEI-----PFSPYY 57
Db 12 LLLAAVPLRAAATLDESG-----GLVSP-----GGSLTLVCKSGGFTFSYG 55

Qy 58 PWELATAPDVIRISWRG--HPHGQSFYSTRPPSIHKDYVNLFLNWTGQKSGFLRISNL 115
Db 56 VSWVRQAPGKLEWAGITDSGGTYTA---PAVK---GRFTISRNNGQSTATLQNSL 108

Qy 116 QKQDOSVYFCRVEL--DTRSGRQWQSIETKLSITQOQRTKATTPAREPQNT--EEP 172
Db 109 KASDTATYCYKAGYAGIRSIDILMG--HTEVAVSSGSTAPSVFPISSCCGSTQQQP 166

Qy 173 YENIRNEGQNTDPKLNPKDDGIVYASLALSSTSPRAPPSH 213
Db 167 VVGCLATGYTGP-----VTFSMGASGATSVTPETH 199

RESULT 3
E27889
Ig heavy chain V region (H18-S415) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: E27889
R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to a d
A/Reference number: A91043; MUID:8630658; PMID:2427335
A/Accession: E27889
A/Molecule type: DNA
A/Residues: 1-118 <CAT>
A/Cross-references: UNIPARC:UPI0000176B69
A/Experimental source: strain Balb/c
A/Note: This sequence was determined from the germline gene
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/15-97/Domain: immunoglobulin homology <IMM>

Query Match 8.3%; Score 101; DB 2; Length 118;
Best Local Similarity 24.8%; Pred. No. 0.14;
Matches 33; Conservative 25; Mismatches 35; Indels 40; Gaps 7;

Qy 34 GVTQPKHLASMGSGVE-----IPFSFYYPWELATAPDVIRISWRGHGPHGQSFYSTRP 86
Db 10 GLVXP-----GSLKLSCAASGITFSDYVYWRQTPDKLEW-----VATIT 52

Qy 87 PSI-----HKQVYNRLFLNWTGQKSGFLRISNLQKQDOSVYFCRVELDTRSS-----GRQ 137
Db 53 DDINVTYSDVSGKFTISRDNAXNNYLQLSLKSEDTAMYC-----TRGSYYVDYGM 107

Qy 138 QWQSIETKLSIT 150
Db 108 YWG--QGTSTVTS 118

RESULT 4
I46626
rearranged T-cell receptor delta-chain/ Vdelta1.4-Ddelta1.4-Jdelta1 - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C/Accession: I46626
R/Yang, Y.G.; Ohta, S.; Yamada, S.; Shimizu, M.; Takagaki, Y.
J. Immunol. 155, 1981-1993, 1995
A/Title: Diversity of T cell receptor delta-chain cDNA in the thymus of a one-month-old
A/Reference number: I46623; MUID:95363165; PMID:7636249
A/Accession: I46626

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-151 <YAN>
A/Cross-references: UNIPARC:UPI000011B2A5; GB:D49567; NID:G1041136; PIDN:BAA08511.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 8.2%; Score 100.5; DB 2; Length 151;
Best Local Similarity 27.7%; Pred. No. 0.2;
Matches 39; Conservative 17; Mismatches 50; Indels 35; Gaps 4;

Qy 6 LLLPPLLPPAPLPQSGSGSPSYLYGVTPQKHLASMGSGSVEIPFSFYYPWELATAP 65
Db 3 LSSLLMLFLTSVP-----SGSGVAQKVTDQQP-VSRQVGEAVTLNCRVETSNVEYTI- 54

Qy 66 DVIRISWRGHGPHGQSFYSTRPPSIHKDYV-----NRLPLNWTGQKSGFLRIS 113
Db 55 -----FWYKQPPSGEMTFLIYQVSASRNAKDGRYFINFQAKQSLSLTIS 99

Qy 114 NLQKQDOSVYFCRVELDTRSS 134
Db 100 ALQLQDSATYFCALWVVTNSS 120

RESULT 5
S25758
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25758
R/Combrinato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25758
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-235 <COM>
A/Cross-references: UNIPARC:UPI0000115F06; EMBL:X57823; NID:q33745; PIDN:CAA40960.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/150-218/Domain: immunoglobulin homology <IMM>

Query Match 8.1%; Score 99; DB 2; Length 235;
Best Local Similarity 28.4%; Pred. No. 0.48;
Matches 44; Conservative 20; Mismatches 59; Indels 32; Gaps 8;

Qy 26 GSGSPSYLYGVTPQKHLASMGSGSVEIPFSFYYPWELATAPDVIRISWRGHGPHGQSFYSTR 85
Db 14 GTGSAQSAQTQAPASVSGSPQSITISCT-----GSSSDV-----GGYNYVSVYQQH 60

Qy 86 PPSIHK-----DYVNL--FLNWTGQKSG---FLRISNLQKQDOSVYFCRVELDTRSSGR 136
Db 61 PGKAPKLMIVDVNRPSPGVSNRPFSGSKSGNTASITISGLQPEDADYYC-----TSKTSS 115

Qy 137 QWQSIETKLSITQOQRTKATT---PAREPQ 167
Db 116 SFYVFGTGKVSUL-GQPKANPTVTLFPSPSEELQ 149

RESULT 6
I38912
receptor tyrosine kinase - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
C/Accession: I38912
R/Crosier, K.E.; Hall, L.R.; Lewis, P.M.; Morris, C.M.; Wood, C.R.; Morris, J.C.; Crosie
Growth Factors 11, 137-144, 1994
A/Title: Isolation and characterization of the human DTK receptor tyrosine kinase.
A/Reference number: I38912; MUID:95161080; PMID:7857658
A/Accession: I38912
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 99.2506 Seconds
(without alignments)
1634.967 Million cell updates/sec

Title: US-10-780-043-4

Perfect score: 1223
Sequence: 1 MGRPLLLPLLLPLPPAFLLQ.....PSHRPLKSPQNETLYSLVLA 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1173.5	96.0	303	Q9UKJ1_HUMAN	Q9ukj1 homo sapien
2	1044	85.4	226	Q8NH11_HUMAN	Q8nh11 homo sapien
3	744	60.8	227	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
4	505.5	41.3	299	Q8BYA6_MOUSE	Q8bya6 mus musculus
5	126	10.3	633	Q5W434_BRARE	Q5w434 brachydanio
6	126	10.3	651	Q5W433_BRARE	Q5w433 brachydanio
7	113.5	9.3	1709	1 SN_HUMAN	Q9bzz2 homo sapien
8	111.5	9.1	233	Q8TBC9_HUMAN	Q8tbc9 homo sapien
9	109.5	9.0	386	Q58DE8_BOVIN	Q58de8 bos taurus
10	109	8.9	1694	1 SN_MOUSE	Q62230 mus musculus
11	109	8.9	1730	Q7YRQ7_PIG	Q7yrg7 sus scrofa
12	106	8.7	400	Q4T054_TETNG	Q4t054 tetraodon n
13	104	8.5	285	Q9JME9_MOUSE	Q9jme9 mus musculus
14	104	8.5	512	Q96DN8_HUMAN	Q96dn8 homo sapien
15	104	8.5	5635	Q5TYR7_HUMAN	Q5tyr7 homo sapien
16	104	8.5	5636	Q9GRW7_HUMAN	Q9grw7 homo sapien
17	103.5	8.5	302	Q4T853_TETNG	Q4t853 tetraodon n
18	102.5	8.4	149	Q63YF8_HUMAN	Q63yf8 homo sapien
19	102.5	8.4	271	Q9HBS0_HUMAN	Q9hbs0 homo sapien
20	102.5	8.4	551	1 SGL5_HUMAN	Q15389 homo sapien
21	102	8.3	236	Q6PIQ7_HUMAN	Q6piq7 homo sapien
22	102	8.3	325	Q501V7_BRARE	Q501v7 brachydanio
23	101	8.3	477	2 Q510J1_RAT	Q510j1 rattus norv
24	99.5	8.1	235	Q6P2J1_HUMAN	Q6p2j1 homo sapien
25	99.5	8.1	870	Q5L6U6_CHLAB	Q5l6u6 chlamydomophi
26	99.5	8.1	1150	2 Q8BS24_MOUSE	Q8bs24 mus musculus
27	98	8.0	394	2 Q6UXG0_HUMAN	Q6uxg0 homo sapien
28	98	8.0	3950	2 Q7VRF5_CANFA	Q7vrf5 canis famil
29	97.5	8.0	416	2 Q7M048_RAT	Q7m048 rattus norv
30	97.5	8.0	439	1 NF1C_MOUSE	Q70255 mus musculus
31	97.5	8.0	595	2 Q5W431_FUGRU	Q5w431 fugu rubrip

32	97.5	8.0	630	2 Q5W436_FUGRU	Q5w436 fugu rubrip
33	97.5	8.0	648	2 Q5W435_FUGRU	Q5w435 fugu rubrip
34	97.5	8.0	1209	2 P70232_MOUSE	P70232 mus musculus
35	97	7.9	142	1 VPRL1_MOUSE	P13372 mus musculus
36	97	7.9	142	2 Q5W1K4_MOUSE	Q5w1k4 mus musculus
37	97	7.9	142	2 Q545E0_MOUSE	Q545e0 m 13 days e
38	97	7.9	487	2 Q8ZVX0_HUMAN	Q8zvx0 homo sapien
39	96.5	7.9	235	2 Q8PUG0_HUMAN	Q8pug0 homo sapien
40	96.5	7.9	235	2 Q99M11_MOUSE	Q99m11 mus musculus
41	96.5	7.9	439	2 Q70188_RAT	Q70188 rattus norv
42	96.5	7.9	479	2 Q7TMK4_MOUSE	Q7tmk4 mus musculus
43	96.5	7.9	7962	2 Q10465_HUMAN	Q10465 homo sapien
44	96.5	7.9	34350	2 Q8WZ42_HUMAN	Q8wz42 homo sapien
45	96	7.8	226	1 CD79A_HUMAN	P11912 homo sapien

ALIGNMENTS

RESULT 1
ID Q9UKJ1_HUMAN PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Inhibitory receptor PILRALpha.
GN Name=PILRA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
"PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is RT paired with the truncated counterpart PILRBeta.";
J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161080; AAD52964.1; -; mRNA.
DR Ensembl; ENSG00000085514; Homo sapiens.
DR HGNC; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; P:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG, 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 303 AA; 33878 MW; 0410ADFC7E80928B CRC64;

Query Match	96.0%;	Score 1173.5;	DB 2;	Length 303;
Best Local Similarity	75.6%;	Pred. No. 7.7e-91;		
Matches 229;	Conservative 1;	Mismatches 0;	Indels 73;	Gaps 1;
QY	1	MGRPLLLPLLLPLPPAFLLQSGSGSPSYLYGVYTOPKHLASMGSGSVEIPFSFYYPWE	60	
Db	1	MGRPLLLPLLLPLPPAFLLQSGSGSPSYLYGVYTOPKHLASMGSGSVEIPFSFYYPWE	60	
QY	61	LATAPDVRLSWRRGHFHGQSFYSTPRPPSIHKDYVNVRLFLNMTWEGQKSGFLRISNLQKQDQ	120	
Db	61	LATAPDVRLSWRRGHFHGQSFYSTPRPPSIHKDYVNVRLFLNMTWEGQKSGFLRISNLQKQDQ	120	
QY	121	SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPPSSMTTWRSLSTTTTGLRV	151	
Db	121	SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPPSSMTTWRSLSTTTTGLRV	180	
QY	152	-----GQORTKATTTPAREPQ	167	
Db	181	TQKRRSDSWHISLSTAVGVAVTVLIGIMILGLICLLRWRRKGGQORTKATTTPAREPQ	240	

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QY 168 NTEPYENIRNEGQNTDPKLNPKDDGIYVYASLALSSSTSPRAPPSPONETLYSV 227
DB 241 NTEPYENIRNEGQNTDPKLNPKDDGIYVYASLALSSSTSPKAPPSPONETLYSV 300
QY 228 LKA 230
DB 301 LKA 303

RESULT 2
Q8NH11 HUMAN
ID Q8NH11 HUMAN PRELIMINARY; PRT; 226 AA.
AC Q8NH11;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PILRA protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Kryzwicki M.I., Skalska U., Smalhus D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the ENBL/GenBank/DBJ databases.
DR EMBL; BC017812; AAH17812.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin domain.
SQ SEQUENCE 226 AA; 25479 MW; 539818197733A30 CRC64;

Query Match 85.4%; Score 1044; DB 2; Length 226;
Best Local Similarity 90.7%; Pred. No. 4.6e-80;
Matches 196; Conservative 6; Mismatches 10; Indels 4; Gaps 1;

QY 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60
DB 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60
QY 61 LATAPDVIRISWRGRGHFGQSFYSTRPPIHKDYVNRFLNWTGQSGFLRISNLKQDQ 120
DB 61 LATAPDVIRISWRGRGHFGQSFYSTRPPIHKDYVNRFLNWTGQSGFLRISNLKQDQ 120
QY 121 SVYFCRVELDTRSSGRQOQWISIEGTKLSITGQOORTKATTPAREPFTQTEPYENIRNEG 180

us-10-780-043-4.rup
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DB 121 SVYFCRVELDTRSSGRQOQWISIEGTKLSITGQOORTKATTPAREPFTQTEPYENIRNEG 180
QY 181 QNTDPKLNPKDDGIYVYASLALSSSTSPRAPPSPHRPL 216
DB 181 QNTDPKLNPK- ---LHLTOSTSQSPQEPERDPV 212

RESULT 3
Q9UKJ0 HUMAN
ID Q9UKJ0 HUMAN PRELIMINARY; PRT; 227 AA.
AC Q9UKJ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Activating receptor PtiRbeta (Hypothetical protein DKFZp434O079).
GN Name=DKFZp434O079;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Barville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PtiRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-
bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
paired with the truncated counterpart PtiRbeta."
RL J. Biol. Chem. 275:4467-4474 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Testis;
RA The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the ENBL/GenBank/DBJ databases.
CC -1- INTERACTION:
CC O95870-BAT5; M5EXP=1; IntAct=EBI-347958, EBI-348517;
DR EMBL; AF161081; AAD52965.1; -; mRNA.
DR EMBL; AL834336; CAH10711.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. . .; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Hypothetical protein; Immunoglobulin domain; Receptor.
SQ SEQUENCE 227 AA; 25542 MW; 7FF960C60AB7BF09 CRC64;

Query Match 60.8%; Score 744; DB 2; Length 227;
Best Local Similarity 86.4%; Pred. No. 1.1e-54;
Matches 140; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60
DB 1 MGRPLLLPLLLPAPLPQSGTSGSPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60
QY 61 LATAPDVIRISWRGRGHFGQSFYSTRPPIHKDYVNRFLNWTGQSGFLRISNLKQDQ 120
DB 61 LATAPDVIRISWRGRGHFGQSFYSTRPPIHKDYVNRFLNWTGQSGFLRISNLKQDQ 120
QY 121 SVYFCRVELDTRSSGRQOQWISIEGTKLSITGQOORTKATTPA 162
DB 121 SVYFCRVELDTRSSGRQOQWISIEGTKLSITGQOORTKATTPA 162

RESULT 4
Q8BYA6_MOUSE
ID Q8BYA6_MOUSE PRELIMINARY; PRT; 299 AA.
AC Q8BYA6;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 23.9707 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-4
Perfect score: 1223
Sequence: 1 MGRPILLPLPPLPAPLQ.....PSHRPLKSPQNETLYSVLKA 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pap.*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pap.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pap.*
- 4: /cgn2_6/prodata/1/iaa/PCUS COMB.pap.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pap.*
- 6: /cgn2_6/prodata/1/iaa/baCkfilea1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	230	2	US-09-869-388-4
2	1176.5	96.2	303	2	US-08-985-950-2
3	1176.5	96.2	303	2	US-09-546-049-2
4	1176.5	96.2	303	2	US-09-869-388-2
5	816	66.7	175	2	US-09-869-388-8
6	759	62.1	226	2	US-09-869-388-10
7	745	60.9	238	2	US-09-149-476-485
8	744	60.8	227	2	US-09-869-388-6
9	517	42.3	101	2	US-09-149-476-754
10	222	18.2	99	2	US-08-985-950-4
11	222	18.2	99	2	US-09-546-049-4
12	113.5	9.3	1709	2	US-09-949-016-10503
13	109.5	9.0	244	2	US-08-918-148-79
14	109.5	9.0	244	2	US-09-138-091A-77
15	102.5	8.4	551	2	US-08-896-537A-2
16	100	8.2	229	2	US-08-751-359-22
17	100	8.2	229	2	US-08-907-146-22
18	100	8.2	284	2	US-09-184-658-40
19	100	8.2	284	2	US-09-504-262D-40
20	98.5	8.1	159	1	US-08-653-402B-2
21	98	8.0	335	2	US-08-875-811-57
22	97.5	8.0	104	2	US-10-083-424-40
23	97	7.9	479	2	US-10-104-047-3871
24	96.5	7.9	143	1	US-08-345-321-8
25	96.5	7.9	1209	2	US-09-130-158A-2
26	96	7.8	226	2	US-09-311-784A-32
27	96	7.8	232	2	US-09-949-016-7589

28 96 7.8 232 2 US-09-949-016-7590 Sequence 7590, Ap
29 95.5 7.8 421 2 US-08-753-628-5 Sequence 5, Appl
30 95.5 7.8 553 1 US-08-661-052-16 Sequence 16, Appl
31 95.5 7.8 553 2 US-09-188-082-16 Sequence 16, Appl
32 95.5 7.8 553 2 US-09-364-088-16 Sequence 16, Appl
33 95.5 7.8 553 2 US-09-102-716-16 Sequence 16, Appl
34 95 7.8 360 2 US-09-907-794A-213 Sequence 213, App
35 95 7.8 360 2 US-09-905-125A-213 Sequence 213, App
36 95 7.8 360 2 US-09-902-775A-213 Sequence 213, App
37 95 7.8 360 2 US-09-906-700-213 Sequence 213, App
38 95 7.8 360 2 US-09-903-603A-213 Sequence 213, App
39 95 7.8 360 2 US-09-904-920A-213 Sequence 213, App
40 95 7.8 360 2 US-09-909-064-213 Sequence 213, App
41 95 7.8 360 2 US-09-905-381A-213 Sequence 213, App
42 95 7.8 360 2 US-09-906-618-213 Sequence 213, App
43 95 7.8 360 2 US-09-906-646-213 Sequence 213, App
44 95 7.8 360 2 US-09-904-462-213 Sequence 213, App
45 95 7.8 360 2 US-09-902-736A-213 Sequence 213, App

ALIGNMENTS

RESULT 1
US-09-869-388-4
; Sequence 4, Application US/09869388
; Patent No. 6774214
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/09/869,388
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IEM PC compatible
; SEQ ID NO 4
; LENGTH: 230
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-869-388-4

Query Match 100.0%; Score 1223; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 3e-110;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGRPILLPLPPLPAPLQPSGSGSYLYGVTPKHLASMGSGSYVEIPSFYYPWE 60
DB 1 MGRPILLPLPPLPAPLQPSGSGSYLYGVTPKHLASMGSGSYVEIPSFYYPWE 60
QY 61 LATAPDVRISWRGRHFHGFQSFYSTHDKYVNRFLNWTGQKSGFLRISNLOKQOQ 120
DB 61 LATAPDVRISWRGRHFHGFQSFYSTHDKYVNRFLNWTGQKSGFLRISNLOKQOQ 120
QY 121 SYVFCRVELDTRSSGRQMQSIEGKLSITQOQRTKATTPAREFPQNTPEYINRNEG 180
DB 121 SYVFCRVELDTRSSGRQMQSIEGKLSITQOQRTKATTPAREFPQNTPEYINRNEG 180
QY 181 QNTDKPLNKDGIYVYASLALSSSTSPRAPPSPHRPLKSPQNETLYSVLKA 230
DB 181 QNTDKPLNKDGIYVYASLALSSSTSPRAPPSPHRPLKSPQNETLYSVLKA 230
RESULT 2
US-08-985-950-2
; Sequence 2, Application US/08985950
; Patent No. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22

;;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-985-950-2

Query Match 96.2%; Score 1176.5; DB 2; Length 303;
Best Local Similarity 75.9%; Pred. No. 1.4e-105;
Matches 230; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

QY 1 MGRLLPLPLPAPFLOPSGSGPSVLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
DB 1 MGRLLPLPLPAPFLOPSGSGPSVLYGVTPQKHLASMGSGVEIPPSFYYPWE 60

QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQKSGFLRISNLQKQDQ 120
DB 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQKSGFLRISNLQKQDQ 120

QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQ----- 151
DB 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRPSSMTTWRLLSSTTTTGLRV 180

QY 152 -----GQORTKATTTPAREPQ 167
DB 181 TQGRKRSDSWHISLETAVGVAVTVLGMILGLICLLRWRRKQQRKATTTPAREPQ 240

QY 168 NTEPFYENIRNEGQNTDKLPKPDGIVYASIALSSSTSPRAPPSHRPLKSPQNETLYSV 227
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QY 228 LKA 230
DB 301 LKA 303

RESULT 3

US-09-546-049-2
; Sequence 2, Application US/09546049
; Patent No. 6479638

;;
; GENERAL INFORMATION:
; APPLICANT: Adema, Gese Jan
; Meyaard, Linde
; Gorman, Daniel M.
; McClanahan, Terrill K.
; Zurawski, Sandra M.
; Zurawski, Gerard
; Lanier, Lewis L.
; Phillips Jr., Joseph H.
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; Related Reagents
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/546,049
; FILING DATE: 10-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-546-049-2

Query Match 96.2%; Score 1176.5; DB 2; Length 303;
Best Local Similarity 75.9%; Pred. No. 1.4e-105;
Matches 230; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

QY 1 MGRLLPLPLPAPFLOPSGSGPSVLYGVTPQKHLASMGSGVEIPPSFYYPWE 60
DB 1 MGRLLPLPLPAPFLOPSGSGPSVLYGVTPQKHLASMGSGVEIPPSFYYPWE 60

QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQKSGFLRISNLQKQDQ 120
DB 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQKSGFLRISNLQKQDQ 120

QY 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQ----- 151
DB 121 SVYFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRPSSMTTWRLLSSTTTTGLRV 180

QY 152 -----GQORTKATTTPAREPQ 167
DB 181 TQGRKRSDSWHISLETAVGVAVTVLGMILGLICLLRWRRKQQRKATTTPAREPQ 240

QY 168 NTEPFYENIRNEGQNTDKLPKPDGIVYASIALSSSTSPRAPPSHRPLKSPQNETLYSV 227

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 23, 2005, 20:40:10 ; Search time 78.2515 Seconds
(without alignments)
1228.101 Million cell updates/sec

Title: US-10-780-043-4
Perfect score: 1223
Sequence: 1 MGRPILLPLPPLPFLQ.....PSHRPLKSPQNETLYSVLKA 230

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications 'AA Main':
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1223	100.0	230	4	US-10-780-043-4 Sequence 4, Appli
2	1218	99.6	230	4	US-10-309-290-110 Sequence 110, Appl
3	1176.5	96.2	303	3	US-09-774-381-58 Sequence 58, Appl
4	1176.5	96.2	303	4	US-10-290-631-2 Sequence 2, Appli
5	1176.5	96.2	303	4	US-10-780-043-2 Sequence 2, Appli
6	1176.5	96.2	303	4	US-10-777-524-2 Sequence 2, Appli
7	1176.5	96.2	303	5	US-10-777-521-2 Sequence 2, Appli
8	1057	86.4	206	4	US-10-309-290-112 Sequence 112, App
9	830	67.9	1012	5	US-10-450-763-30868 Sequence 30868, A
10	830	67.9	1012	5	US-10-450-763-33210 Sequence 33210, A
11	830	67.9	1012	5	US-10-450-763-47228 Sequence 47228, A
12	830	67.9	1012	5	US-10-450-763-51762 Sequence 51762, A
13	816	66.7	175	4	US-10-780-043-8 Sequence 8, Appli
14	785	62.6	226	3	US-09-745-763-106 Sequence 106, App
15	759	62.1	226	3	US-09-774-381-44 Sequence 44, Appl
16	759	62.1	226	4	US-10-780-043-10 Sequence 10, Appl
17	745	60.9	238	3	US-09-809-391-485 Sequence 485, App
18	745	60.9	238	3	US-09-882-171-485 Sequence 485, App
19	745	60.9	238	4	US-10-164-861-485 Sequence 485, App
20	744	60.8	227	4	US-10-262-445-128 Sequence 128, App
21	744	60.8	227	4	US-10-780-043-6 Sequence 6, Appli
22	744	60.8	227	5	US-10-820-474A-7 Sequence 7, Appli
23	744	60.8	291	3	US-09-935-390A-21 Sequence 21, Appl
24	744	60.8	326	4	US-10-276-774-2380 Sequence 2380, Ap
25	517	42.3	101	3	US-09-809-391-754 Sequence 754, App
26	517	42.3	101	3	US-09-882-171-754 Sequence 754, App
27	517	42.3	101	4	US-10-164-861-754 Sequence 754, App

28 354 28.9 224 3 US-09-866-050A-711 Sequence 711, App
29 222 18.2 99 4 US-10-290-631-4 Sequence 4, Appli
30 222 18.2 99 4 US-10-777-524-4 Sequence 4, Appli
31 222 18.2 99 5 US-10-777-521-4 Sequence 4, Appli
32 120.5 9.9 124 5 US-10-788-625-92 Sequence 92, Appli
33 116.5 9.5 253 4 US-10-479-670-184 Sequence 184, App
34 115.5 9.4 247 4 US-10-479-670-158 Sequence 158, App
35 115.5 9.4 1700 3 US-09-863-776-24 Sequence 24, Appli
36 114.5 9.4 252 4 US-10-479-670-168 Sequence 168, App
37 114.5 9.4 253 4 US-10-479-670-174 Sequence 174, App
38 114.5 9.4 253 4 US-10-779-461-18 Sequence 18, Appl
39 113.5 9.3 1694 4 US-10-203-708-36 Sequence 36, Appl
40 113.5 9.3 1709 3 US-09-870-759-51 Sequence 51, Appl
41 113.5 9.3 1709 3 US-09-751-708A-51 Sequence 51, Appl
42 113.5 9.3 1709 3 US-09-863-776-58 Sequence 58, Appl
43 113.5 9.3 1709 3 US-09-863-776-60 Sequence 60, Appl
44 113.5 9.3 1709 4 US-10-203-708-35 Sequence 35, Appl
45 113.5 9.3 1709 4 US-10-408-765A-1562 Sequence 1562, Ap

ALIGNMENTS

RESULT 1

US-10-780-043-4
; Sequence 4, Application US/10780043
; Publication No. US20040137506A1
; GENERAL INFORMATION:
; APPLICANT: Bates, Elizabeth
; APPLICANT: Fournier, Nathalie
; APPLICANT: Chalus, Lionel
; APPLICANT: Garrone, Pierre
; TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METH
; FILE REFERENCE: SF0977X
; CURRENT APPLICATION NUMBER: US/10/780,043
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US/09/869,388
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: IBM PC compatible
; SEQ ID NO 4
; LENGTH: 230
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-780-043-4

Query Match 100.0%; Score 1223; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 2.8e-100; Mismatches 0; Indels 0; Gaps 0;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGRPILLPLPPLPFLQPSGSGSYLYGVTPKHLASMGSGSVIPIPSFYYPWE 60
Db 1 MGRPILLPLPPLPFLQPSGSGSYLYGVTPKHLASMGSGSVIPIPSFYYPWE 60
Qy 61 LATADPVRISWRGHFGHQSFPSTPPSIHKDYVRLFLNWTGQSGFLRISNLKQDQ 120
Db 61 LATADPVRISWRGHFGHQSFPSTPPSIHKDYVRLFLNWTGQSGFLRISNLKQDQ 120
Qy 121 SVYFCRVELDTSSGRQWQSTEGTKLSITQOQRTKATTPAREPQNTPEEPYENIRNEG 180
Db 121 SVYFCRVELDTSSGRQWQSTEGTKLSITQOQRTKATTPAREPQNTPEEPYENIRNEG 180
Qy 181 QNTDPKLPKODGIYVYASIALSSSTSPRAPPSHRLKSPQNETLYSVLKA 230
Db 181 QNTDPKLPKODGIYVYASIALSSSTSPRAPPSHRLKSPQNETLYSVLKA 230

RESULT 2

US-10-309-290-110
; Sequence 110, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.

APPLICANT: Anderson, David W.
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Chillakuru, Rajeev A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
APPLICANT: Gould-Rothberg, Bonnie E.
APPLICANT: Guo, Xiaojia
APPLICANT: Jeffers, Michael E.
APPLICANT: Ji, Weizhen
APPLICANT: Li, Li
APPLICANT: Malyankar, Uriel M.
APPLICANT: Miller, Charles E.
APPLICANT: Murphey, Ryan
APPLICANT: Patturajan, Meera
APPLICANT: Peyman, John A.
APPLICANT: Rastelli, Luca
APPLICANT: Rieger, Daniel K.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Smithson, Glenda
APPLICANT: Starling, Gary
APPLICANT: Taupier, Raymond J.
APPLICANT: Voss, Edward Z.
APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/336,600
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,285
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/341,346
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/341,540
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/342,592
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/344,297
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/373,288
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/380,981
PRIOR FILING DATE: 2002-05-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 274
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 110
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-290-110

Query Match 99.6%; Score 1218; DB 4; Length 230;
Best Local Similarity 99.6%; Pred. No. 7.7e-100;
Matches 229; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGRLLLLPPLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60
Db 1 MGRLLLLPPLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60

Qy 61 LATAPDVRIWRGRGHFGQSFYSTPPSIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGRGHFGQSFYSTPPSIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120

Qy 121 SVYFCRVELDRSSGRQMQSIEGTKLSITQGGQRTKATTPAREPFONTPEPYENIRNEG 180

Db 121 SVYFCRVELDRSSGRQMQSIEGTKLSITQGGQRTKATTPAREPFONTPEPYENIRNEG 180

Qy 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPSHRPLKSPQNETLYSVLKA 230
Db 181 QNTDPKLNPKDDGIVYASLALSSSTSPRAPSHRPLKSPQNETLYSVLKA 230

RESULT 3
US-09-774-381-58
Sequence 58, Application US/09774381
Publication No. US20030082677A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: McCarthy, Sean A.
APPLICANT: Pan, Yang
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL EDIPF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
FILE REFERENCE: MNI-107CP2
CURRENT APPLICATION NUMBER: US/09/774,381
CURRENT FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 08/941,354
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/010,674
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/061,149
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 09/014,347
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: 60/061,159
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 09/474,151
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 09/004,206
PRIOR FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 60/061,143
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 09/483,414
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: 09/213,571
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,890
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 303
TYPE: PRT
ORGANISM: Homo sapiens
US-09-774-381-58

Query Match 96.2%; Score 1176.5; DB 3; Length 303;
Best Local Similarity 75.9%; Pred. No. 5.3e-96;
Matches 230; Conservative 0; Mismatches 0; Indels 73; Gaps 1;

Qy 1 MGRLLPPLPPLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60
Db 1 MGRLLPPLPPLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60

Qy 61 LATAPDVRIWRGRGHFGQSFYSTPPSIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGRGHFGQSFYSTPPSIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120

Qy 121 SVYFCRVELDRSSGRQMQSIEGTKLSITQGGQRTKATTPAREPFONTPEPYENIRNEG 151
Db 121 SVYFCRVELDRSSGRQMQSIEGTKLSITQGGQRTKATTPAREPFONTPEPYENIRNEG 151

Qy 152

Db 181 TQGRSDSWHISLETAVGVAVATVVGIMLIGLICLLWRRRKGGQRTKATTPAREPFQ 167

Qy 168 NTEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPSHRPLKSPQNETLYSV 227

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:41:30 ; Search time 4.35831 Seconds
(without alignments)
376.418 Million cell updates/sec

Title: US-10-780-043-4

Perfect score: 1223

Sequence: 1 MGRPILLPLPPLPPLPFLQ.....PSHRPLKSPQNTLYSLVLA 230

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_New.*

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- 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
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- 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113.5	9.3	1649	6	US-10-995-561-974
2	113.5	9.3	1694	7	US-11-135-855-36
3	113.5	9.3	1709	6	US-10-995-561-973
4	113.5	9.3	1709	7	US-11-135-855-35
5	112.5	9.2	258	6	US-10-512-184-26
6	112.5	9.2	327	6	US-10-512-184-62
7	112.5	9.2	328	6	US-10-512-184-63
8	112.5	9.2	328	6	US-10-512-184-64
9	112.5	9.2	576	6	US-10-512-184-65
10	112.5	9.2	625	6	US-10-512-184-47
11	110.5	9.0	246	7	US-11-054-515-2077
12	110.5	9.0	246	7	US-11-054-515-2079
13	108.5	8.9	256	7	US-11-054-515-907
14	106.5	8.7	250	6	US-10-512-184-27
15	106	8.7	250	7	US-11-054-515-1319
16	106	8.7	258	7	US-11-054-515-1841
17	103	8.4	251	7	US-11-054-515-1827
18	102.5	8.4	250	7	US-11-054-515-3247
19	102.5	8.4	252	7	US-11-054-515-1021
20	102.5	8.4	551	7	US-11-000-463-346
21	102	8.3	245	7	US-11-054-515-1864
22	102	8.3	247	7	US-11-054-515-1751
23	102	8.3	250	7	US-11-054-515-837
24	102	8.3	250	7	US-11-054-515-867
25	102	8.3	250	7	US-11-054-515-1313

26	101.5	8.3	252	7	US-11-054-515-1787	Sequence 1787, Ap
27	100.5	8.2	242	7	US-11-054-515-1884	Sequence 1884, Ap
28	100.5	8.2	249	7	US-11-054-515-540	Sequence 540, App
29	100.5	8.2	254	7	US-11-054-515-1525	Sequence 1525, Ap
30	100.5	8.2	256	7	US-11-054-515-2080	Sequence 2080, Ap
31	100	8.2	250	7	US-11-054-515-1561	Sequence 1561, Ap
32	100	8.2	251	7	US-11-054-515-1046	Sequence 1046, Ap
33	100	8.2	251	7	US-11-054-515-1052	Sequence 1052, Ap
34	100	8.2	251	7	US-11-054-515-1053	Sequence 1053, Ap
35	99.5	8.1	249	7	US-11-054-515-708	Sequence 708, App
36	99	8.1	247	7	US-11-054-515-1704	Sequence 1704, Ap
37	99	8.1	249	7	US-11-054-515-2065	Sequence 2065, Ap
38	99	8.1	250	7	US-11-054-515-868	Sequence 868, App
39	99	8.1	250	7	US-11-054-515-933	Sequence 933, App
40	99	8.1	250	7	US-11-054-515-942	Sequence 942, App
41	99	8.1	251	7	US-11-054-515-852	Sequence 852, App
42	99	8.1	251	7	US-11-054-515-879	Sequence 879, App
43	99	8.1	251	7	US-11-054-515-940	Sequence 940, App
44	99	8.1	251	7	US-11-054-515-1047	Sequence 1047, Ap
45	99	8.1	251	7	US-11-054-515-1064	Sequence 1064, Ap

ALIGNMENTS

RESULT 1

US-10-995-561-974
; Sequence 974, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 974
; LENGTH: 1649
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-974

Query Match 9.3%; Score 113.5; DB 6; Length 1649;
Best Local Similarity 24.2%; Pred. No. 0.021;
Matches 46; Conservative 32; Mismatches 85; Indels 27; Gaps 9;
QY 10 LPILLPPALPQSGTSGPSYLYGVTPQKLSASMGSGVEIPFSPYPMELATAPDVRI 69
DB 4 LPKILLASFPFAGQAS-----WGVSPQDVQGVKSGCLLIPCFSPFADVEVPDGIYA 57
QY 70 SWRRGHFHGQS---FYSTRPPSIHKDYNNRL-FLNWTBQKSGFLRISLNKQDOSVYFC 125
DB 58 IWYI-DYSGQRQVWSHSDPKLVEARFRGRTFMGNPEHRVCNLL-LKDLQPEDSSSYNF 115
QY 126 RVELTRSGRQWOSIEGTKLSITQCGQRTKATTPAREPFONTE-----EPY-----EN 175
DB 116 REFI-----SEVNRWSDVKGTLVTVEPRVPTIASPV-ELLEGTVEYDFNCSTPYVCLQSQ 170
QY 176 IRNEGQNTDP 185
DB 171 VRLQWQQDP 180

RESULT 2

US-11-135-855-36
; Sequence 36, Application US/11135855
; Publication No. US2005025557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM p.l.c.


```

; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 1694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-36

Query Match          9.3%; Score 113.5; DB 7; Length 1694;
Best Local Similarity 24.2%; Pred. No. 0.021;
Matches 46; Conservative 32; Mismatches 85; Indels 27; Gaps 9;

Qy 10 LPKLLPAPFLOPSGSGSYLYGVTPQKHLASMGSGVEIPFSPFYPWELATAPDVRI 69
Db 4 LPKLLLASFPFAGQAS-----WGVSSPDQVQVKGSCLLIPCFISFPADVVPDGITA 57

Qy 70 SWRGHFGQS---FYSTRPSIHKDYVNL-FLNWTEGQSGFLRISNLQKQDSVYFC 125
Db 58 IWYI-DYSGQRQVSHSADPKLVEARFRGRTEFMGNPHEHVCNLL-LKDLPEDSGSYNF 115

Qy 126 RVELDTRSSGRQWQSIQTKLSITQGGRTKATTPAREPFQNT-----EPY-----EN 175
Db 116 RFEI-----SEVNRWSDVKGLTVVTEPRVPTIASPV-ELLEGTVDVDFNCSTPYVCLQEQ 170

Qy 176 IRNEGQNTDP 185
Db 171 VRLQWQGDQ 180

RESULT 3
US-10-995-561-973
; Sequence 973, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 973
; LENGTH: 1709
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-973

Query Match          9.3%; Score 113.5; DB 6; Length 1709;
Best Local Similarity 24.2%; Pred. No. 0.022;
Matches 46; Conservative 32; Mismatches 85; Indels 27; Gaps 9;

Qy 10 LPKLLPAPFLOPSGSGSYLYGVTPQKHLASMGSGVEIPFSPFYPWELATAPDVRI 69
Db 4 LPKLLLASFPFAGQAS-----WGVSSPDQVQVKGSCLLIPCFISFPADVVPDGITA 57

Qy 70 SWRGHFGQS---FYSTRPSIHKDYVNL-FLNWTEGQSGFLRISNLQKQDSVYFC 125
Db 58 IWYI-DYSGQRQVSHSADPKLVEARFRGRTEFMGNPHEHVCNLL-LKDLPEDSGSYNF 115
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Qy 126 RVELDTRSSGRQWQSIQTKLSITQGGRTKATTPAREPFQNT-----EPY-----EN 175
Db 116 RFEI-----SEVNRWSDVKGLTVVTEPRVPTIASPV-ELLEGTVDVDFNCSTPYVCLQEQ 170

Qy 176 IRNEGQNTDP 185
Db 171 VRLQWQGDQ 180

RESULT 4
US-11-135-855-35
; Sequence 35, Application US/11135855
; Publication No. US20050255557A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50013
; CURRENT APPLICATION NUMBER: US/11/135,855
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US/10/203,708
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/04703
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,172
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/186,084
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 1709
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-135-855-35

Query Match          9.3%; Score 113.5; DB 7; Length 1709;
Best Local Similarity 24.2%; Pred. No. 0.022;
Matches 46; Conservative 32; Mismatches 85; Indels 27; Gaps 9;

Qy 10 LPKLLPAPFLOPSGSGSYLYGVTPQKHLASMGSGVEIPFSPFYPWELATAPDVRI 69
Db 4 LPKLLLASFPFAGQAS-----WGVSSPDQVQVKGSCLLIPCFISFPADVVPDGITA 57

Qy 70 SWRGHFGQS---FYSTRPSIHKDYVNL-FLNWTEGQSGFLRISNLQKQDSVYFC 125
Db 58 IWYI-DYSGQRQVSHSADPKLVEARFRGRTEFMGNPHEHVCNLL-LKDLPEDSGSYNF 115

Qy 126 RVELDTRSSGRQWQSIQTKLSITQGGRTKATTPAREPFQNT-----EPY-----EN 175
Db 116 RFEI-----SEVNRWSDVKGLTVVTEPRVPTIASPV-ELLEGTVDVDFNCSTPYVCLQEQ 170

Qy 176 IRNEGQNTDP 185
Db 171 VRLQWQGDQ 180

RESULT 5
US-10-512-184-26
; Sequence 26, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Forderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 258
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:18:33 ; Search time 126.054 Seconds
(without alignments)
1056.147 Million cell updates/sec

Title: US-10-780-043-2
Perfect score: 1591
Sequence: 1 MGRPLLLPLLLPLPPAPLQ.....PSHRLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_21.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003s.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*
 - 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1591	100.0	303	2	Aaw62772 Human imm
2	1591	100.0	303	2	Aab07443 A human m
3	1588	99.8	303	8	Adp25129 PRO polyp
4	1176.5	73.9	230	3	Aab07444 A human m
5	1171.5	73.6	230	7	Adp95578 Human NOV
6	1010.5	63.5	206	7	Adp95580 Human NOV
7	973.5	61.2	226	2	Aay08015 Human LSP
8	973.5	61.2	226	3	Aab07447 A human m
9	967.5	60.8	226	5	Aaw80407 A secrete
10	967.5	60.8	226	5	Abp61825 Human pol
11	958	60.2	227	3	Aab07445 A human m
12	958	60.2	227	6	Abu89824 TNF-recep
13	958	60.2	291	2	Aaw63682 Human sec
14	958	60.2	326	4	Abb12010 Human sec
15	945	59.4	227	3	Aay87230 Human sig
16	934	58.7	238	5	Abg95345 Human nov
17	934	58.7	238	6	Abg034539 Region of
18	934	58.7	238	8	Adh74202 Human sec
19	927.5	58.3	228	8	Adk98565 Human imm
20	927.5	58.3	228	8	Adk98565 Human imm
21	821	51.6	175	3	Aab07446 A human m
22	808	50.8	1012	4	Abg00509 Novel hum
23	808	50.8	1012	4	Abg16869 Novel hum
24	808	50.8	1012	4	Abg02851 Novel hum

25	808	50.8	1012	4	ABG211403	Novel hum
26	517	32.5	101	2	AAW75053	Fragment
27	517	32.5	101	5	ABG95614	Human nov
28	517	32.5	101	6	ABO34808	Fragment
29	517	32.5	101	7	AD123469	Novel hum
30	517	32.5	101	8	ADH74471	Human sec
31	411	25.8	224	5	ABG72387	Murine pr
32	405.5	25.5	212	7	ABE59537	Rat Prote
33	222	14.0	99	2	AAW62773	Partial m
34	148.5	9.3	305	4	AAU14284	Human nov
35	148.5	9.3	305	9	ABE11270	Human KIL
36	146.5	9.2	305	4	AAU14520	Human nov
37	146.5	9.2	305	4	ABG66271	Human TAN
38	146.5	9.2	305	5	AAU08796	Human leu
39	146.5	9.2	305	5	AAO19216	Human sec
40	146.5	9.2	305	8	ADS11833	Human the
41	146.5	9.2	305	8	ADS11832	Human the
42	146.5	9.2	305	8	ADS11831	Human the
43	146.5	9.2	305	8	ADS10561	Human the
44	145.5	9.1	305	8	ADH80838	Human pol
45	139	8.7	290	4	AAW74712	Human mem

ALIGNMENTS

RESULT 1
AAW62772
ID AAW62772 standard; protein; 303 AA.
XX AC AAW62772;
XX DT 23-SEP-1998 (first entry)
XX DE Human immunoglobulin receptor designated FDF03.
XX KW Human; type I transmembrane protein; immunoglobulin-like domain; FDF03;
XX KW activated monocyte; YE01; KTE03; control; development; differentiation;
XX KW mammalian immune system; treatment; cancerous condition;
XX KW degenerative condition; autoimmune response; transplantation rejection;
XX KW graft versus host disease; inflammatory condition; detection; diagnosis;
XX KW drug screening.
XX OS Homo sapiens.
XX PN WO9824906-A2;
XX PD 11-JUN-1998.

XX PF 05-DEC-1997; 97WO-US021101.
XX PR 06-DEC-1996; 96US-0032252P.
XX PR 09-DEC-1996; 96US-00762187.
XX PR 16-DEC-1996; 96US-0033181P.
XX PR 21-MAR-1997; 97US-0041279P.
XX (SCHE) SCHERING CORP.

XX PI Adena CJ, Meygaard L, Gorman DM, Mcclanahan TK, Zurawski SM;
XX PI Zurawski G, Lanier LL, Phillips JH;
XX DR WPI; 1998-333325/29.
XX DR N-PSDB; AAV38987.

XX PT New isolated activated monocyte cell gene(s) - used to develop products
XX PT for treating e.g. cancer, degenerative conditions, autoimmune responses,
XX PT transplant rejection or inflammatory conditions.
XX PS Claim 1; Page 60-61; 104pp; English.

XX CC The present sequence represents a human protein, FDF03, which is a type I
XX CC transmembrane protein comprising an extracellular portion characterised
XX CC by immunoglobulin-like domains, indicating that the protein is a receptor

CC member of the immunoglobulin superfamily. The FDF03 gene is found in
 CC activated monocytes. The specification also describes other proteins
 CC encoded by activated monocytes, which are designated YE01 and KTE03. The
 CC genes function in controlling development, differentiation, and/or
 CC physiology of the mammalian immune system. The products can be used for
 CC treating abnormal proliferation, regeneration, degeneration or atrophy.
 CC They can be used for treating e.g. Cancerous conditions, degenerative
 CC conditions, autoimmune responses, transplantation rejection, graft versus
 CC host disease, or inflammatory conditions. The products can also be used
 CC for detection, diagnosis and drug screening

XX SQ Sequence 303 AA;

Query Match 100.0%; Score 1591; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 7.7e-122;
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60
 Db 1 MGRPLLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60

Qy 61 LATAPDVRIISWRGHFGQSPYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKQDQ 120
 Db 61 LATAPDVRIISWRGHFGQSPYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKQDQ 120

Qy 121 SVYFCRVELDTRSSGRQMQSIEGTKLSTQAVTTTTPRPSMTTWRLSSTTTTGLRV 180
 Db 121 SVYFCRVELDTRSSGRQMQSIEGTKLSTQAVTTTTPRPSMTTWRLSSTTTTGLRV 180

Qy 181 TOGKRSDSWHISLETAVGAVAVTVLIGIMILGICLLRWRRRKGQRTKATTPAREPFQ 240
 Db 181 TOGKRSDSWHISLETAVGAVAVTVLIGIMILGICLLRWRRRKGQRTKATTPAREPFQ 240

Qy 241 NTEPEYINRNEGQNTDPLNPKDDGIVYASLASLSSTSPRAPSHRPLKSPQNETLYSV 300
 Db 241 NTEPEYINRNEGQNTDPLNPKDDGIVYASLASLSSTSPRAPSHRPLKSPQNETLYSV 300

Qy 301 LKA 303
 Db 301 LKA 303

RESULT 2

AA07443
 ID AAB07443 standard; protein; 303 AA.

AC AAB07443;

XX 20-OCT-2000 (first entry)

XX A human monocyte-derived protein FDF03.

XX Human, monocyte-derived protein; FDF03; FDF03DeltaTM; FDF03-S1;
 KW FDF03-M14; FDF03-S2; haematopoietic cell; monocyte hyperplasia;
 KW tissue rejection; inflammation; infection.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT Protein 20..303
 FT Protein /note= "mature protein"

XX MO200040721-A1.

XX 13-JUL-2000.

XX 29-DEC-1999; 99WO-US030004.

XX 31-DEC-1998; 98US-00223919.

XX 31-DEC-1998; 98US-00224604.

XX

PA (SCHE) SCHERING CORP.

XX Bates E, Fournier N, Chaulus L, Garrone P;

XX WPI; 2000-465984/40.

DR N-PSDB; AAA58814.

XX Novel monocyte-derived polypeptides and polynucleotides, used to diagnose
 PT diseases associated with changes in monocyte numbers, e.g. bacterial or
 PT viral infections.

XX Claim 1; Page 32-33; 45pp; English.

XX The present sequence represents a human monocyte-derived protein. The
 CC specification describes monocyte-derived proteins FDF03, FDF03DeltaTM,
 CC FDF03-S1, FDF03-M14, and FDF03-S2. The proteins are involved in the
 CC regulation, or development, of haematopoietic cells. Antibodies specific
 CC for antigenic components of the proteins can be used to detect the
 CC components in samples. The proteins can also be used to screen for
 CC candidate therapeutic agents. The monocyte-derived proteins and
 CC polynucleotides can be used for diagnosis of diseases related to an
 CC increase, or decrease, in the number of monocytes in a tissue or lymph
 CC system, such as monocyte hyperplasia, tissue or graft rejection,
 CC inflammation, or bacterial or viral infections. The proteins can also be
 CC used in the treatment of disorders associated with abnormal expression or
 CC signalling by a monocyte

XX SQ Sequence 303 AA;

Query Match 100.0%; Score 1591; DB 3; Length 303;
 Best Local Similarity 100.0%; Pred. No. 7.7e-122;
 Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGRPLLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60

Db 1 MGRPLLLPLLLPAPLQPSGSGPSYLYGVTPKHLASMGSGVEIPFSFYFWE 60

Qy 61 LATAPDVRIISWRGHFGQSPYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKQDQ 120

Db 61 LATAPDVRIISWRGHFGQSPYSTRPPIHDKYVNRFLNWTGQKSGFLRISNLQKQDQ 120

Qy 121 SVYFCRVELDTRSSGRQMQSIEGTKLSTQAVTTTTPRPSMTTWRLSSTTTTGLRV 180

Db 121 SVYFCRVELDTRSSGRQMQSIEGTKLSTQAVTTTTPRPSMTTWRLSSTTTTGLRV 180

Qy 181 TOGKRSDSWHISLETAVGAVAVTVLIGIMILGICLLRWRRRKGQRTKATTPAREPFQ 240

Db 181 TOGKRSDSWHISLETAVGAVAVTVLIGIMILGICLLRWRRRKGQRTKATTPAREPFQ 240

Qy 241 NTEPEYINRNEGQNTDPLNPKDDGIVYASLASLSSTSPRAPSHRPLKSPQNETLYSV 300

Db 241 NTEPEYINRNEGQNTDPLNPKDDGIVYASLASLSSTSPRAPSHRPLKSPQNETLYSV 300

Qy 301 LKA 303

Db 301 LKA 303

RESULT 3

ADP25129

ID ADP25129 standard; protein; 303 AA.

XX ADP25129;

XX 18-NOV-2004 (first entry)

XX PRO polypeptide SEQ ID NO:2307.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antiproliferative; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
 XX Unidentified.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:20:23 ; Search time 31.5788 Seconds
(without alignments)
793.277 Million cell updates/sec

Title: US-10-780-043-2

Perfect score: 1591

Sequence: 1 MGRPILLPLPPLPAPFLQ.....PSHRPLKSPQNETLYSVLKA 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/prodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/prodata/1/1aa/H COMB.pep.*
4: /cgn2_6/prodata/1/1aa/PCITUS COMB.pep.*
5: /cgn2_6/prodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1591	100.0	303	2	US-08-985-950-2
2	1591	100.0	303	2	US-09-546-049-2
3	1591	100.0	303	2	US-09-869-388-2
4	1176.5	73.9	230	2	US-09-869-388-4
5	973.5	61.2	226	2	US-09-869-388-10
6	958	60.2	227	2	US-09-869-388-6
7	934	58.7	238	2	US-09-149-476-485
8	821	51.6	175	2	US-09-869-388-8
9	517	32.5	101	2	US-09-149-476-754
10	222	14.0	99	2	US-08-985-950-4
11	222	14.0	99	2	US-09-546-049-4
12	130.5	8.2	431	2	US-09-038-832-2
13	130.5	8.2	431	2	US-09-038-832-4
14	130.5	8.2	447	2	US-09-949-016-8211
15	119	7.5	341	2	US-09-336-536-29
16	119	7.5	370	2	US-09-336-536-28
17	114	7.2	390	1	US-08-979-424-1
18	114	7.2	390	2	US-09-907-794A-39
19	114	7.2	390	2	US-09-905-125A-39
20	114	7.2	390	2	US-09-302-775A-39
21	114	7.2	390	2	US-09-906-700-39
22	114	7.2	390	2	US-09-903-603A-39
23	114	7.2	390	2	US-09-904-920A-39
24	114	7.2	390	2	US-09-909-064-39
25	114	7.2	390	2	US-09-905-381A-39
26	114	7.2	390	2	US-09-906-618-39
27	114	7.2	390	2	US-09-906-646-39

Query Match 100.0%; Score 1591; DB 2; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.5e-141;

ALIGNMENTS

RESULT 1

US-08-985-950-2
; Sequence 2, Application US/08985950
; Patent No. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181
; FILING DATE: 16-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-950-2

28 114 7.2 390 2 US-09-904-462-39 Sequence 39, Appl
29 114 7.2 390 2 US-09-902-736A-39 Sequence 39, Appl
30 114 7.2 390 2 US-09-906-722A-39 Sequence 39, Appl
31 114 7.2 417 2 US-09-949-016-6729 Sequence 6729, Ap
32 114 7.2 456 2 US-09-949-016-7564 Sequence 7564, Ap
33 113.5 7.1 319 1 US-08-597-495B-22 Sequence 22, Appl
34 113.5 7.1 319 2 US-09-068-051A-22 Sequence 22, Appl
35 113.5 7.1 319 2 US-09-336-536-67 Sequence 67, Appl
36 113.5 7.1 319 2 US-09-254-465A-6 Sequence 6, Appl
37 113.5 7.1 319 2 US-09-953-499-6 Sequence 6, Appl
38 113 7.1 316 2 US-09-397-243D-13 Sequence 13, Appl
39 111.5 7.0 306 2 US-09-369-247-63 Sequence 63, Appl
40 111.5 7.0 306 2 US-10-062-548-63 Sequence 63, Appl
41 110.5 6.9 244 2 US-08-918-148-79 Sequence 79, Appl
42 110.5 6.9 244 2 US-09-138-091A-77 Sequence 77, Appl
43 110 6.9 300 1 US-08-661-052-4 Sequence 4, Appl
44 110 6.9 300 2 US-09-188-082-4 Sequence 4, Appl
45 110 6.9 300 2 US-09-364-088-4 Sequence 4, Appl

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Qy	1	MGRPLLLPLLLPAPFLQPSGTS	GGPSYLYGVTPQKHL	SASMG	SVIPIPSFY	PWE	60			
Db	1	MGRPLLLPLLLPAPFLQPSGTS	GGPSYLYGVTPQKHL	SASMG	SVIPIPSFY	PWE	60			
Qy	61	LATAPDVRISWRRGHFGQSFY	STRPPSIHKDYVNRFL	PLNWT	EQQKSGFLRIS	NLQKQD	120			
Db	61	LATAPDVRISWRRGHFGQSFY	STRPPSIHKDYVNRFL	PLNWT	EQQKSGFLRIS	NLQKQD	120			
Qy	121	SVYFCRVELDTRSGRQOMOSI	EGTKLSIITQAVTTTT	QRPSSMTT	WRLS	TTTTTGLRV	180			
Db	121	SVYFCRVELDTRSGRQOMOSI	EGTKLSIITQAVTTTT	QRPSSMTT	WRLS	TTTTTGLRV	180			
Qy	181	TQGRSDSHI	SLETAGVAVAVTV	LGIMILGLICLL	RRRRK	GQORTKATTPARE	PFQ	240		
Db	181	TQGRSDSHI	SLETAGVAVAVTV	LGIMILGLICLL	RRRRK	GQORTKATTPARE	PFQ	240		
Qy	241	NTEEPYENIRNEQNTD	PKLNPKDDGIVYAS	LALSS	TS	PRAPSPHRLKSPQN	ETIY	SV	300	
Db	241	NTEEPYENIRNEQNTD	PKLNPKDDGIVYAS	LALSS	TS	PRAPSPHRLKSPQN	ETIY	SV	300	
Qy	301	LKA	303							
Db	301	LKA	303							

RESULT 2

US-09-546-049-2
 / Sequence 2, Application US/09546049
 / Patent No. 6479638
 / GENERAL INFORMATION:
 / APPLICANT: Adema, Gosse Jan
 / Meysaard, Linde
 / Gorman, Daniel M.
 / McClanahan, Terrill K.
 / Zurawski, Sandra M.
 / Zurawski, Gerard
 / Lanier, Lewis L.
 / Phillips Jr., Joseph H.
 / TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;

RESULT 3
US-09-869-388-2
; Sequence 2: Application us/09869388

Query Match	100.00%	Score 1591;	DB 2;	Length 303;
Best Local Similarity	100.00%	Pred. No. 1.5e-141;		
Matches 303;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MGRPLLLPLLLPLPAFLQPSGSGTSGPSYLYGVTPQKHLASMSGSGSVEIPSPFPY	60
Db	1	MGRPLLLPLLLPLPAFLQPSGSGTSGPSYLYGVTPQKHLASMSGSGSVEIPSPFPY	60
Qy	61	LATAPDVRISWRGHPHGQSFYSTRPPSIHKQVYVNFLEFNWTEGQSGGFLRISNLQKQDQ	120
Db	61	LATAPDVRISWRGHPHGQSFYSTRPPSIHKQVYVNFLEFNWTEGQSGGFLRISNLQKQDQ	120
Qy	121	SVYFCRVELDTRSSGRQOWSGTEGTXLSITQAVTTTTTORPSSMTTWRLSSTTTTTTGLRV	180

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:40:10 ; Search time 103.088 Seconds
(without alignments)
1228.101 Million cell updates/sec

Title: US-10-780-043-2

Perfect score: 1591

Sequence: 1 MGRPLLLPLLLPLPPAFLQ.....PSHRPLKSPQNETLYSLVKA 303

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1591	100.0	303	3	US-09-774-381-58
2	1591	100.0	303	4	US-10-290-631-2
3	1591	100.0	303	4	US-10-780-043-2
4	1591	100.0	303	4	US-10-777-524-2
5	1591	100.0	303	5	US-10-777-521-2
6	1176.5	73.9	230	4	US-10-780-043-4
7	1171.5	73.6	230	4	US-10-309-290-110
8	1010.5	63.5	206	4	US-10-309-290-112
9	973.5	61.2	226	3	US-09-774-381-44
10	973.5	61.2	226	4	US-10-780-043-10
11	967.5	60.8	226	3	US-09-745-763-106
12	958	60.2	227	4	US-10-262-445-128
13	958	60.2	227	4	US-10-780-043-6
14	958	60.2	227	5	US-10-820-474A-7
15	958	60.2	291	3	US-09-935-390A-21
16	958	60.2	326	4	US-10-276-774-2380
17	934	58.7	238	3	US-09-809-391-485
18	934	58.7	238	3	US-09-882-171-485
19	934	58.7	238	4	US-10-164-861-485
20	821	51.6	175	4	US-10-780-043-8
21	808	50.8	1012	5	US-10-450-763-30868
22	808	50.8	1012	5	US-10-450-763-33210
23	808	50.8	1012	5	US-10-450-763-47228
24	808	50.8	1012	5	US-10-450-763-51762
25	517	32.5	101	3	US-09-809-391-754
26	517	32.5	101	3	US-09-882-171-754
27	517	32.5	101	4	US-10-164-861-754

28	411	25.8	224	3	US-09-866-050A-711	Sequence 711, App
29	222	14.0	99	4	US-10-290-631-4	Sequence 4, Appl
30	222	14.0	99	4	US-10-777-524-4	Sequence 4, Appl
31	222	14.0	99	5	US-10-777-521-4	Sequence 4, Appl
32	148.5	9.3	305	4	US-10-291-265-391	Sequence 391, App
33	148.5	9.3	305	5	US-10-727-012-3	Sequence 3, Appl
34	148.5	9.3	305	5	US-10-962-127-3	Sequence 3, Appl
35	148.5	9.3	305	5	US-10-962-127-58	Sequence 58, Appl
36	146.5	9.2	305	3	US-09-796-753-104	Sequence 104, App
37	146.5	9.2	305	3	US-09-796-753-120	Sequence 120, App
38	146.5	9.2	305	4	US-10-291-265-863	Sequence 863, App
39	139	8.7	290	3	US-09-965-529-18	Sequence 18, Appl
40	139	8.7	290	3	US-09-969-680A-18	Sequence 18, Appl
41	139	8.7	290	4	US-10-227-884-40	Sequence 40, Appl
42	139	8.7	290	4	US-10-230-163-40	Sequence 40, Appl
43	139	8.7	290	4	US-10-230-338-40	Sequence 40, Appl
44	139	8.7	290	4	US-10-218-631-40	Sequence 40, Appl
45	139	8.7	290	4	US-10-230-414-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1

US-09-774-381-58
; Sequence 58, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL EDIFR, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-107CP2
; CURRENT APPLICATION NUMBER: US/09/774,381
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-381-58

Query Match 100.0%; Score 1591; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 6.6e-126;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPLLLPLPPAFLQSGPSVLYGVYTOPKHLASMGGSVEIPFSYVYDRE 60
|||||

Db 1 MGRPLLLPLLLPAPLQPSGSGSPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60
QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120
QY 121 SVYFCRVELDTSSGRQMQSIEGTKLSITQAVTTTTPRPSSMTTWRLSSTTTTGLRV 180
Db 121 SVYFCRVELDTSSGRQMQSIEGTKLSITQAVTTTTPRPSSMTTWRLSSTTTTGLRV 180
QY 181 TOGKRSDSWHISLETAVGAVAVTVLGMILGLICLLRWRRRKQOQRTKATTPAREPFQ 240
Db 181 TOGKRSDSWHISLETAVGAVAVTVLGMILGLICLLRWRRRKQOQRTKATTPAREPFQ 240
QY 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRLPLKSPQNETLYSV 300
Db 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRLPLKSPQNETLYSV 300
QY 301 LKA 303
Db 301 LKA 303

RESULT 2

US-10-290-631-2
Sequence 2, Application US/10290631
Publication No. US20030105303A1

GENERAL INFORMATION:

APPLICANT: Adema, Gosse Jan

Meygaard, Linde

Gorman, Daniel M.

McClanahan, Terrill K.

Zurawski, Sandra M.

Zurawski, Gerard

Lanier, Lewis L.

Phillips Jr., Joseph H.

TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;

Related Reagents

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/290,631

FILING DATE: 08-NO. US20030105303A1-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/985,950

FILING DATE: 05-DEC-1997

APPLICATION NUMBER: US 60/041,279

FILING DATE: 21-MARCH-1997

APPLICATION NUMBER: US 60/033,181

FILING DATE: 16-DEC-1996

APPLICATION NUMBER: US 60/032,252

FILING DATE: 06-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0670K

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650)852-9196

TELEFAX: (650)496-1204

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-290-631-2

Query Match 100.0%; Score 1591; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 6.6e-126;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPLLLPAPLQPSGSGSPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60
Db 1 MGRPLLLPLLLPAPLQPSGSGSPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60
QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120
QY 121 SVYFCRVELDTSSGRQMQSIEGTKLSITQAVTTTTPRPSSMTTWRLSSTTTTGLRV 180
Db 121 SVYFCRVELDTSSGRQMQSIEGTKLSITQAVTTTTPRPSSMTTWRLSSTTTTGLRV 180
QY 181 TOGKRSDSWHISLETAVGAVAVTVLGMILGLICLLRWRRRKQOQRTKATTPAREPFQ 240
Db 181 TOGKRSDSWHISLETAVGAVAVTVLGMILGLICLLRWRRRKQOQRTKATTPAREPFQ 240
QY 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRLPLKSPQNETLYSV 300
Db 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLALSSSTSPRAPPSHRLPLKSPQNETLYSV 300
QY 301 LKA 303
Db 301 LKA 303

RESULT 3

US-10-780-043-2

Sequence 2, Application US/10780043

Publication No. US20040137506A1

GENERAL INFORMATION:

APPLICANT: Bates, Elizabeth

APPLICANT: Fournier, Nathalie

APPLICANT: Chalus, Lionel

APPLICANT: Garrone, Pierre

TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS

FILE REFERENCE: SF0977X

CURRENT APPLICATION NUMBER: US/10/780,043

CURRENT FILING DATE: 2004-02-17

PRIOR APPLICATION NUMBER: US/09/869,388

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: IBM PC compatible

SEQ ID NO 2

LENGTH: 303

TYPE: PRT

ORGANISM: homo sapiens

US-10-780-043-2

Query Match 100.0%; Score 1591; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 6.6e-126;
Matches 303; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPLLLPAPLQPSGSGSPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60
Db 1 MGRPLLLPLLLPAPLQPSGSGSPSYLVGTQPKHLSASMGSGVPIPSFYYPWE 60
QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120
Db 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHKDYVNRFLFNWTEGQSGFLRISNLQKQDQ 120
QY 121 SVYFCRVELDTSSGRQMQSIEGTKLSITQAVTTTTPRPSSMTTWRLSSTTTTGLRV 180

Db 1 MLLTLTLLLPWL-----SGYIVTQITGPTTVNGLRGLSLVQCVRSGWETYLK-- 51
QY 67 VRISWRGHPHQSFYSTRPPSIHKDYVNRFLNWTGQKSGFLRIS--NLQKQDQSVYF 124
Db 52 ---WRCGAIWRDCKILVKTSGSQE-VKRDVSIKDNQKRTFTVTMEDLMKTDADTYW 107
QY 125 CRVELDTRSSGRQOQSIQEGTKLSITQAVT---TTTQRPSSMTTW-----RLSSTT 173
Db 108 CGIEK-----TGNDLGVTVQVITDPAFTPTTSTTFTAPVQETSSSP 154
QY 174 TTTGLRVTQKRRSDSHISLETAVGAVAVATVGLIMILGLICLLRWRKGGQORTKATT 233
Db 155 TLTG-----HHLDRHKLKLSVLLPLIFTIL-LLLVAASLLAWRMKYOQKAAGMS 206
QY 234 PAR--EPQNTTEBYENIRNEGQNTDP-----KLN-----PKDDGIVY 269
Db 207 PEQVLQPLEG-DLCYADLTQLAGTSRKATTKLSAQAQDVQVEVYVTMASLPKED-ISKY 264
QY 270 ASIALSSTSTSPRAP-----PSHRPLKSPQNETLYSVL 301
Db 265 ASLTIGA--EDQEPYCNMGLSHSLPGRGPPEPTEYSTI 302

RESULT 2

US-11-000-463-863
; Sequence 863, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radcoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 863
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-863

Query Match 9.2%; Score 146.5; DB 7; Length 305;
Best Local Similarity 23.5%; Pred. No. 7.6e-06;
Matches 80; Conservative 51; Mismatches 126; Indels 83; Gaps 16;
QY 7 LPLPLLLPAPFLOPQSGTSGPSYLYGVTPKHLASMGSGSVIPIPSFYFWMELATPD 66
Db 1 MLLTLTLLLPWL-----SGYIVTQITGPTTVNGLRGLSLVQCVRSGWETYLK-- 51

QY 67 VRISWRGHPHQSFYSTRPPSIHKDYVNRFLNWTGQKSGFLRIS--NLQKQDQSVYF 124
Db 52 ---WRCGAIWRDCKILVKTSGSQE-VKRDVSIKDNQKRTFTVTMEDLMKTDADTYW 107
QY 125 CRVELDTRSSGRQOQSIQEGTKLSITQAVT---TTTQRPSSMTTW-----RLSSTT 173
Db 108 CGIEK-----TGNDLGVTVQVITDPAFTPTTSTTFTAPVQETSSSP 154
QY 174 TTTGLRVTQKRRSDSHISLETAVGAVAVATVGLIMILGLICLLRWRKGGQORTKATT 233
Db 155 TLTG-----HHLDRHKLKLSVLLPLIFTIL-LLLVAASLLAWRMKYOQKAAGMS 206
QY 234 PAR--EPQNTTEBYENIRNEGQNTDP-----KLN-----PKDDGIVY 269
Db 207 PEQVLQPLEG-DLCYADLTQLAGTSRKATTKLSAQAQDVQVEVYVTMASLPKED-ISKY 264
QY 270 ASIALSSTSTSPRAP-----PSHRPLKSPQNETLYSVL 301
Db 265 ASLTIGA--EDQEPYCNMGLSHSLPGRGPPEPTEYSTI 302

RESULT 3

US-11-000-463-377
; Sequence 377, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radcoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 377
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-377

Query Match 7.6%; Score 121; DB 7; Length 406;
Best Local Similarity 24.7%; Pred. No. 0.0017;
Matches 74; Conservative 37; Mismatches 130; Indels 58; Gaps 13;
QY 5 LLLPLLLPAPFLOPQSGTSGPSYLYGVTPKHLASMGSGSVIPIPSFYFWMELATA 64
Db 3 LLLPLLLPMTGKME--GDRQYGDGYLLQVQZ--LVTQVEGLCVHVPSCSFYDQDWD 58
QY 65 PD-VRISWRGHPHQSGFYSTRPPSIHKDYVNRFLNWTGQ-----KSGFLRIS 114


```
Qy 224 KQOQRTK-----ATTAPREFFQNTBEPYENIRNEGQNTDPKLNPKDD 265
      :      :      :      :      :      :      :      :
Db 533 RENPDDENLPHAIISGPDLLNPNKPNQ-----ENATPLNPNPDD 571

RESULT 2
T49517
p63 related protein [imported] - Neurospora crassa
N/Alternate names: protein B14D6.690
C/Species: Neurospora crassa
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
R/Schulte, U.; Align, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A/Reference number: 225022
A/Accession: T49517
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1114 <SCH>
A/Cross-references: UNIPARC:UPI0000179E4B; EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.690
A/Experimental source: BAC clone B14D6; strain OR74A
C/Genetics:
A/Gene: NCSP:B14D6.690
A/Map position: 6
A/Introns: 132/2; 362/2; 427/3; 540/3

Query Match 7.8%; Score 123.5; DB 2; Length 1114;
Best Local Similarity 23.1%; Pred. No. 0.14;
Matches 66; Conservative 32; Mismatches 81; Indels 107; Gaps 12;

Qy 26 GSGPSYLYGVTPQPKHLSASMGSGVEIPFSPYWPWELATAPDVIRISWRGHFHGQSPFYSTR 85
      :      :      :      :      :      :      :      :
Db 155 GSDPADL-----ATWISDDKDFMFY-----APLIQINMQS-----SDR 188

Qy 86 PPSIHKDYVNRFLNFWTEGQKSGFLRISNLQKQOSVYFCRVELDTSSGRQMQWSIEGT 145
      :      :      :      :      :      :      :      :
Db 189 P-----TETVPSGTVSL-----VDVDTMST-----LAT 212

Qy 146 KLSITQAVTTTQRPSSMTTWRLSSITTTTGLRVTOGKRSDSMH-LSLETA--GVAV 202
      :      :      :      :      :      :      :      :
Db 213 AGDAPAGVTSKVPFSOSVVLVGSQGNKPTG--ASEGNKEEDGVKVPVSJSTGPKVGMAV 270

Qy 203 AVTVLIGIMILGLICLLWRRRKQQR-----TKATTPAREPFFONTE----- 243
      :      :      :      :      :      :      :      :
Db 271 AGGVLAIVAIIIFICAWRRKQKQMBEEDPMYGMKDVGVSTADFRNEETPGWHRGPT 330

Qy 244 -----EPYENIRNEGQNTDPKLNPKDDGIVVASLALSSTSPRAPPS 285
      :      :      :      :      :      :      :      :
Db 331 RQPPAPVDPRSDGES-----ELMAPPAPYHPPS 359

RESULT 3
JC5288
SHP substrate-1 protein, 509 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C/Accession: JC5288
R/Yamao, T.; Matoraki, T.; Amano, K.; Matsuda, Y.; Takahashi, N.; Ochi, F.; Fujioka, Y.;
Biochem. Biophys. Res. Commun. 231, 61-67, 1997
A/Title: Mouse and human SHPS-1: Molecular cloning of cDNAs and chromosomal localization
A/Reference number: JC5287; MUID:97223399; PMID:9070220
A/Contents: Brain
A/Accession: JC5288
A/Molecule type: mRNA
A/Residues: 1-509 <YAM>
A/Cross-references: UNIPARC:UPI000002A265; DBJ:D87967; NID:gl864012; FIDN:BAAL3520.1; F
C/Comment: This protein is a glycosylated receptor-like protein and plays a role in cell
acts as a docking protein and induce translocation of SHP-2 from the cytosol to the pla
C/Genetics:
A/Gene: shps-1
A/Map position: 2

Query Match 7.4%; Score 118.5; DB 2; Length 509;
```

```
Best Local Similarity 22.9%; Pred. No. 0.14;
Matches 57; Conservative 44; Mismatches 83; Indels 65; Gaps 13;

Qy 56 YYPWELATADPVIRISWRGHFHGQSPFYSTRPPIHDKDYVNRFLNFWTEGQKSGFLRISNL 115
      :      :      :      :      :      :      :      :
Db 279 FYP-----EDLQILWLE---NGVSRNDTPKNTKN-----TDGTYNTSLFLVNSSA 323

Qy 116 QKODQSVYFCRVELDTSSGRQMQWSIEGTKLISITQAVTTTQRPSSMTTWRLSSITTT 175
      :      :      :      :      :      :      :      :
Db 324 HRD-VVFTQVQVHD-----QQ-----PAITRN-----HTVLGLAHSSDQ 357

Qy 176 TGLRVTOGKRSDSMHISLETAAGVAVATVVLGIMILGLICLLWRRRKQQRKTATTPA 235
      :      :      :      :      :      :      :      :
Db 358 GSNQTFPGNNAATHMNV---FIGVGACALLVLLMAALYLLRIKQKAKGSTST--- 410

Qy 236 REPPQNTBEPYENIRNEGQNTDPKLNPKDDGIVVASLAL---SSSTSPRAPPSHRPLKSPQ 293
      :      :      :      :      :      :      :      :
Db 411 -----RLHEPEKNAREITQID--TNDIND-ITYADLNLPKPKKPAPRAP-----EPN 455

Qy 294 NETLYSVLK 302
      :      :      :
Db 456 NHTYEASIE 464

RESULT 4
B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C/Species: Cercopithecus aethiops (green monkey, grivet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: B44194
R/Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no puta
A/Reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: B44194
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-392 <KOI>
A/Cross-references: UNIPROT:P32506; UNIPARC:UPI000002B1F7; GB:S48817
C/Superfamily: poliovirus receptor; immunoglobulin homology
F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 7.3%; Score 116; DB 2; Length 392;
Best Local Similarity 21.2%; Pred. No. 0.15;
Matches 77; Conservative 42; Mismatches 110; Indels 134; Gaps 16;

Qy 4 PLLPLPLPLLLPAPLQPSGSTGSPSYLYGVTPQPKHLSASMGSGVEIPFSPYWPWELAT 63
      :      :      :      :      :      :      :      :
Db 11 PLLLTLLLELWPP-----PGTGDII---VOAPTQVPGFLGDSVTLPCYLQVPGMEET 59

Qy 64 APDVRISWRGHFHGQS-----FYSTRPPIHDKDYVNRFLNFWTEGQKSGF----- 109
      :      :      :      :      :      :      :      :
Db 60 HVS-QLTWSR---HGSGSMVAFHQTOGP-----NYSEPKRLBFAARLGTTEL 103

Qy 110 ----LRISNLQKQDSYVFC-----RVELDTSSGRQMQWSIEGTKLIS 149
      :      :      :      :      :      :      :      :
Db 104 RDSLRMFLGRVEDEGNYTCLFVTFPGSRSVDIWLRLVLAQPNTAEVQVQLTGKVPV 163

Qy 150 TQAVTTTQRPSSMTTWIR-----LSSTTTTGLRVTOGKRSDS----- 189
      :      :      :      :      :      :      :      :
Db 164 ARCVSTGGRPPAHI--TWHSDLGCMPTNSQAPGFLSGTIVTISLWILVPSQVDGKSVTC 221

Qy 190 --WHISLETAAGVAVATVVLGIMILGLICLLWRRRKQQRKTATTPAREPFFONTEPYE 247
      :      :      :      :      :      :      :      :
Db 222 KVEHSEKPKQLLVNLTIVY-----YPPFVSIISGYD 252

Qy 248 N-----IRNEGQNT-DPKLNPKDDGIVVASLALSSTSPRAPPSH-----RPLKSPQ 293
      :      :      :      :      :      :      :      :
Db 253 NNWYLSQNEATLTCDARSNEPTGYNW-----STTMGPLPPFAVAQAQALLIRPVDKPI 306

Qy 294 NET 296
      :      :
Db 307 NTT 309
```

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OM protein - protein search, using sw model

Run on: December 23, 2005, 20:19:13 ; Search time 130.752 Seconds
(without alignments)
1634.967 Million cell updates/sec

Title: US-10-780-043-2

Perfect score: 1591

Sequence: 1 MGRPLLLPPLPPLPAPFLQ.....PSHRPLKSPQNETLYSLVLA 303

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1588	99.8	303	Q9UKJ1_HUMAN	Q9ukj1 homo sapien
2	997.5	62.7	226	Q8NH11_HUMAN	Q8nh11 homo sapien
3	958	60.2	227	Q9UKJ0_HUMAN	Q9ukj0 homo sapien
4	630	39.6	299	Q8BYA6_MOUSE	Q8bya6 mus musculus
5	144.5	9.1	823	AXL2_YEAST	P38928 saccharomyc
6	139	8.7	290	Q6UX24_HUMAN	Q6ux24 homo sapien
7	139	8.7	290	Q726A6_HUMAN	Q726a6 homo sapien
8	136	8.5	290	Q8TDQ1_HUMAN	Q8tdq1 homo sapien
9	135.5	8.5	293	Q72715_HUMAN	Q72715 homo sapien
10	130.5	8.2	499	SIGL8_HUMAN	Q9ny24 homo sapien
11	130	8.2	289	Q6OX35_MOUSE	Q6ox35 mus musculus
12	129.5	8.1	233	Q8TEC9_HUMAN	Q8tec9 homo sapien
13	127	8.0	283	Q5DMN6_EPTBU	Q5dmn6 eptatretus
14	123.5	7.8	328	Q6ZMC9_HUMAN	Q6zmc9 homo sapien
15	123.5	7.8	353	Q7SDQ5_NEUCR	Q7sdq5 neurospora
16	123.5	7.8	858	Q5TVT7_BRARE	Q5tv77 brachydanio
17	122.5	7.7	235	Q9SM11_MOUSE	Q9sm11 mus musculus
18	122	7.7	288	Q46707_FUGRU	Q46707 fugu rubrip
19	122	7.7	367	Q4GUE4_FUGRU	Q4gue4 fugu rubrip
20	121.5	7.6	633	Q5W434_BRARE	Q5w434 brachydanio
21	121.5	7.6	651	Q5W433_BRARE	Q5w433 brachydanio
22	120	7.5	236	Q6PIQ7_HUMAN	Q6piq7 homo sapien
23	120	7.5	283	Q5DMN5_EPTBU	Q5dmn5 eptatretus
24	119.5	7.5	434	Q872V2_NEUCR	Q872v2 neurospora
25	119	7.5	318	Q91B03_SPERC	Q91b03 spheeroides
26	117.5	7.4	235	Q6P2J1_HUMAN	Q6p2j1 homo sapien
27	117.5	7.4	366	Q46705_FUGRU	Q46705 fugu rubrip
28	116	7.3	417	PVR_CBRAE	P32506 cercopithec
29	115.5	7.3	513	SH2P1_MOUSE	P97797 m tyrosine-
30	115	7.2	367	Q46706_FUGRU	Q46706 fugu rubrip
31	114.5	7.2	235	Q6P790_HUMAN	Q6p790 homo sapien

32 114.5 7.2 283 2 Q5DMN4_EPTBU Q5dmn4 eptatretus
33 114 7.2 390 1 B5AM_HUMAN B5am11 homo sapien
34 114 7.2 417 1 PVR_HUMAN P15151 homo sapien
35 113.5 7.1 319 2 G3A33_HUMAN G99795 homo sapien
36 113.5 7.1 319 2 Q5VZP6_HUMAN Q5vzp6 homo sapien
37 113.5 7.1 387 1 SIG13_FANTR Q64ja4 pan troglod
38 113 7.1 283 2 Q5DMN2_EPTBU Q5dmn2 eptatretus
39 113 7.1 401 2 Q88835_CERAE Q88835 cercopithec
40 113 7.1 718 2 O73675_XENLA O73675 xenopus lae
41 113 7.1 718 2 Q6PCK4_XENLA Q6pck4 xenopus lae
42 112.5 7.1 403 1 CD33_MOUSE Q63994 mus musculus
43 112.5 7.1 700 2 Q8TG00_ASPFU Q8tg00 aspergillus
44 112.5 7.1 700 2 Q4WS89_ASPFU Q4ws89 aspergillus
45 112.5 7.1 1795 2 O76894_DROME O76894 drosophila

ALIGNMENTS

RESULT 1
ID Q9UKJ1_HUMAN PRELIMINARY; PRT; 303 AA.
AC Q9UKJ1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Inhibitory receptor PILRALpha.
GN Name=PILRA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10660620; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRALpha, a novel immunoreceptor tyrosine-based inhibitory motif-bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is paired with the truncated counterpart PILRBeta.";
RL J. Biol. Chem. 275:4467-4474(2000).
DR EMBL; AF161080; AAS2964.1; -; mRNA.
DR Ensembl; ENSG0000085514; Homo sapiens.
DR HGNC; HGNC:20396; PILRA.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005515; P:protein binding; ISS.
DR GO; GO:0007171; P:transmembrane receptor protein tyrosine kin. .; ISS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 303 AA; 33878 MW; 0410ADFC7E80928B CRC64;

Query Match 99.8%; Score 1588; DB 2; Length 303;
Best Local Similarity 99.7%; Pred. No. 9.3e-124;
Matches 302; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGRPLLLPPLPPLPAPFLQSGSGPSYLYGVYTOPKHLASMSGSGVEIPFSFYYPWE 60
DB 1 MGRPLLLPPLPPLPAPFLQSGSGPSYLYGVYTOPKHLASMSGSGVEIPFSFYYPWE 60
QY 61 LATADPVRISWRGRGHFGQSFYSTPRPSIHKDYVNRFLNLTWTEGQKSGFLRISLNKQDQ 120
DB 61 LATADPVRISWRGRGHFGQSFYSTPRPSIHKDYVNRFLNLTWTEGQKSGFLRISLNKQDQ 120
QY 121 SYVFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRSPSSMTTWRLSSITTTTGLRV 180
DB 121 SYVFCRVELDTRSSGRQWQSIETGKLSITQAVTTTTPRSPSSMTTWRLSSITTTTGLRV 180
QY 181 TQGRKRSDSWHLSLETAVGVAVTVLGMIMLGLICLLRWRRKKGQORTKATTPAREPQ 240
DB 181 TQGRKRSDSWHLSLETAVGVAVTVLGMIMLGLICLLRWRRKKGQORTKATTPAREPQ 240

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QY 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLASLSSSTSPRAPSHRPLKSPQNETLYSV 300
DB 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLASLSSSTSPRAPSHRPLKSPQNETLYSV 300
QY 301 LKA 303
DB 301 LKA 303

RESULT 2
Q8NH1L HUMAN
ID Q8NH1L HUMAN PRELIMINARY; PRT; 226 AA.
AC Q8NH1L;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PILRA protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Kryzinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017812; AAH17812.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 226 AA; 25479 MW; 5938181797733A30 CRC64;

Query Match 62.7%; Score 997.5; DB 2; Length 226;
Best Local Similarity 67.8%; Pred. No. 8.7e-75;
Matches 196; Conservative 6; Mismatches 10; Indels 77; Gaps 2;

QY 1 MGRPLLLPLLLPAPLPQSGTSGPSYLYGVTPQKHLASMGSGSVEIPFSFYYPWE 60
DB 1 MGRPLLLPLLLPAPLPQSGTSGPSYLYGVTPQKHLASMGSGSVEIPFSFYYPWE 60
QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHDKYVNRFLFNWTEGQSGFLRISNLQKQD 120
DB 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHDKYVNRFLFNWTEGQSGFLRISNLQKQD 120
QY 121 SVYFCRVELDTSRSGRQOQWSIEGTKLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
DB 121 SVYFCRVELDTSRSGRQOQWSIEGTKLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
QY 121 SVYFCRVELDTSRSGRQOQWSIEGTKLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180

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DB 121 SVYFCRVELDTSRSGRQOQWSIEGTKLSITQ----- 151
QY 181 TOGKRSDSWHISLETAVGVAVVTVLIGLILCLLRWRKRGQORTKATTPAREPFG 240
DB 152 -----GQORTKATTPAREPFG 167
QY 241 NTEEPYENIRNEGQNTDPKLNPKDDGIVYASLASLSSSTSPRAPSHRPL 289
DB 168 NTEEPYENIRNEGQNTDPKLNPK-----LHLTQSTSQPPSPQEPFERDPV 212

RESULT 3
Q9UKJ0 HUMAN
ID Q9UKJ0 HUMAN PRELIMINARY; PRT; 227 AA.
AC Q9UKJ0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Activating receptor PILRbeta (Hypothetical protein DKFZp434O079).
GN Name=DKFZp434O079;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20127940; PubMed=10606020; DOI=10.1074/jbc.275.6.4467;
RA Mousseau D.D., Banville D., L'Abbe D., Bouchard P., Shen S.H.;
RT "PILRalpha, a novel immunoreceptor tyrosine-based inhibitory motif-
RT bearing protein, recruits SHP-1 upon tyrosine phosphorylation and is
RT paired with the truncated counterpart PILRbeta."
RL J. Biol. Chem. 275:4467-4474 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -I- INTERACTION:
CC Q95870:BATS; NbExp=1; IntAct=EBI-347958, EBI-348517;
DR EMBL; AF161081; AAD52565.1; -; mRNA.
DR EMBL; AL834336; CAH10711.1; -; mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Hypothetical protein; Immunoglobulin domain; Receptor.
SQ SEQUENCE 227 AA; 25542 MW; 7FF960C60A57EF09 CRC64;

Query Match 60.2%; Score 958; DB 2; Length 227;
Best Local Similarity 80.8%; Pred. No. 1.7e-71;
Matches 185; Conservative 15; Mismatches 19; Indels 10; Gaps 2;

QY 1 MGRPLLLPLLLPAPLPQSGTSGPSYLYGVTPQKHLASMGSGSVEIPFSFYYPWE 60
DB 1 MGRPLLLPLLLPAPLPQSGTSGPSYLYGVTPQKHLASMGSGSVEIPFSFYYPWE 60
QY 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHDKYVNRFLFNWTEGQSGFLRISNLQKQD 120
DB 61 LATAPDVRIWRGRGHFGQSFYSTRPPIHDKYVNRFLFNWTEGQSGFLRISNLQKQD 120
QY 121 SVYFCRVELDTSRSGRQOQWSIEGTKLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
DB 121 SVYFCRVELDTSRSGRQOQWSIEGTKLSITQAVTTTQRPSSMTTWRLSSTTTTGLRV 180
QY 181 TOGKRSDSWHISLETAVGVAVVTVLIGLILCLLR-----WRRRKQOQ 227

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